

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 10, 2004, 11:55:42 ; Search time 5327 Seconds
(without alignments)
10740.155 Million cell updates/sec

Title: US-09-430-775-1

Perfect score: 1320
Sequence: 1 AGTATTGTTGTCGTTTGC.....CCAGCATCTCGCTTTCTG 1320

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vl.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

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30: em_htg_hum.*

31: em_htg_inv.*

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34: em_htg_pln.*

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36: em_htg_mam.*

37: em_htg_vrt.*

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39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1320	100.0	1320	6	AR075909 Sequence
2	1320	100.0	1320	6	AR083195 Sequence
3	1320	100.0	1320	6	I20778 Sequence 1
4	1304.8	98.8	75031	9	AL390716 Human DNA
5	1300	98.5	1452	9	Z66526 H.sapiens p
6	1283.6	97.2	1673	9	U42387 Human pancr
7	1210	91.7	53269	2	AC006184 Homo sapi
8	1180	89.4	1180	6	AR270498 Sequence
9	1180	89.4	1180	6	U35232 Human neuro
10	1128	85.5	1128	6	AX548917 Sequence
11	1120	84.8	1128	9	AY268432 Homo sapi
12	1051.2	79.6	1128	9	AY149475 Macaca mu
13	982.6	74.4	1796	4	AB021678 Sus scrof
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16	811.2	61.5	224691	2	AC129870 Rattus no
17	811.2	61.5	249291	2	AC109718 Rattus no
18	810.8	61.4	1439	6	AR083220 Sequence
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23	780.6	59.1	1209	10	RNPPIGN Z68180 R.norvegicu
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25	451.6	34.2	1134	5	AF410853 Gallus ga
26	417.8	31.7	1315	5	AF073925 Gadus mor
27	364	27.6	1098	5	AF340022 Lampetra
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30	303	23.0	1149	10	MMU58367 Z18280 Mus musculu
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ALIGNMENTS

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LOCUS AR075909 1320 bp DNA linear PAT 30-AUG-2000
DEFINITION Sequence 1 from patent US 5958709.
ACCESSION AR075909
VERSION AR075909.1 GI:10002655
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1320)
AUTHORS Eard, J.A., Walker, M.W., Branchek, T. and Weinschenk, R.L.
TITLE Processes for identifying compounds that bind to the human Y4
receptor
JOURNAL Patent: US 5958709-A 1 28-SEP-1999;

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Best Local Similarity 100.0%; Pred. No. 2.7e-227;
Matches 1320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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LOCUS             1320 bp      DNA      linear      PAT 01-SEP-2000
DEFINITION       Sequence 1 from patent US 5976814.
ACCESSION        AR083195
VERSION          AR083195.1  GI:10009985
KEYWORDS         Unknown.
SOURCE           Unknown.
ORGANISM         Unknown.
REFERENCE        1 (bases 1 to 1320)
AUTHORS          Bard, J.A., Walker, M.W., Branchek, T. and Weinshank, R.L.
TITLE            DNA encoding a human neuropeptide Y/peptide YY/pancreatic
                polypeptide receptor (YY) and uses thereof
JOURNAL          Patent: US 5976814-A 1 02-NOV-1999;
FEATURES         Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.7e-227;
Matches 1320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
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DEFINITION Sequence 1 from patent US 5516653.
ACCESSION 120778
VERSION 120778.1 GI:1601133

KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1320)
AUTHORS Bard, J.A., Walker, M.W., Branchek, T. and Weinshank, R.L.
TITLE DNA encoding a human neuropeptide Y/peptide YY/pancreatic polypeptide receptor (Y4) and uses thereof
JOURNAL Patent: US 5516653-A 1 14-MAY-1996;
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Best Local Similarity 100.0%; Pred. No. 2.7e-227;
Matches 1320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 6
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LOCUS Human pancreatic polypeptide receptor mRNA, complete cds.
DEFINITION U42387
ACCESSION U42387
VERSION U42387.1 GI:1314327
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1673)
Yan, H., Yang, J., Marasco, J., Yamaguchi, K., Brenner, S., Collins, F.
and Karbon, W.
Cloning and functional expression of cDNAs encoding human and rat
pancreatic polypeptide receptors
Proc. Natl. Acad. Sci. U.S.A. 93 (10), 4661-4665 (1996)
96209788
MEDLINE 8643460
PUBMED 2 (bases 1 to 1673)
Yan, H., Yang, J., Marasco, J., Yamaguchi, K., Brenner, S., Collins, F.
and Karbon, W.
Direct Submision
Submitted (07-DEC-1995) Hai Yan, Neuroscience, Amgen Inc., 1840
DeHavilland Drive, Thousand Oaks, CA 91326, USA
JOURNAL Location/Qualifiers
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LOCUS AR270498 1180 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 1061 from patent US 6500938.
ACCESSION AR270498
VERSION AR270498.1 GI:29701732
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1180)
AUTHORS Au-Yang, J. and Seilhamer, J. J.
TITLE Composition for the detection of signaling pathway gene expression
JOURNAL Patent: US 6500938-A 1061 31-DEC-2002;
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Best Local Similarity 100.0%; Pred. No. 4e-202;
Matches 1180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 9
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LOCUS HSU35232
DEFINITION Human neuropeptide Y4 receptor protein gene, complete cds.
ACCESSION U35232
VERSION U35232.1 GI:1063629
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1180)
AUTHORS Bard, J. A., Walker, M. W., Branchek, T. A. and Weinshank, R. L.
TITLE Cloning and functional expression of a human Y4 subtype receptor for pancreatic polypeptide, neuropeptide Y, and peptide YY

J. Biol. Chem. 270 (45), 26762-26765 (1995)
MEDLINE 96070761
PUBMED 7592911
REFERENCE 2 (bases 1 to 1180)
AUTHORS Bard, J. A.
TITLE Direct Submission
JOURNAL Submitted (31-AUG-1995) Jonathan A. Bard, Molecular Biology,
Synaptic Pharmaceutical Corporation, 215 College Rd., Paramus, NY
07652, USA
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Matches 1180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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LOCUS AX548917 1128 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 202 from Patent WO02061087.
ACCESSION AX548917
VERSION AX548917.1 GI:25813768
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Burmer, G.C., Roush, C.L. and Brown, J.P.
TITLE Antigenic peptides, such as for G protein-coupled receptors (GPCRs), antibodies thereto, and systems for identifying such antigenic peptides
JOURNAL Patent: WO 02061087-A 202 08-AUG-2002;
Lifespan Biosciences, Inc. (US)
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Best Local Similarity 100.0%; Pred. No. 8.8e-193;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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DEFINITION AF072822
ACCESSION AF072822
VERSION AF072822.1 GI:4235258
KEYWORDS Cavia porcellus (domestic guinea pig)
SOURCE Cavia porcellus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
REFERENCE Eriksson H., Berglund, M.M., Holmberg, S.K., Kahl, U., Gehlert, D.R.
AUTHORS and Larhammar, D.
TITLE The cloned guinea pig pancreatic polypeptide receptor Y4 resembles
more the human Y4 than does the rat Y4
JOURNAL Regul. 75-76, 29-37 (1998)
MEDLINE 99017377
PUBMED 9802391
REFERENCE Sharma, P.S., Holmberg, S.K., Eriksson, H., Beck-Sickinger, A.G.,
AUTHORS Grundemar, L., and Larhammar, D.

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TITLE Direct Submission
JOURNAL Submitted (22-JUN-1998) Neuroscience, Uppsala University, Box 593,
Uppsala S-75124, Sweden
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Job time : 5337 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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ALIGNMENTS

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XX therapeutic; ss.
XX Homo sapiens.
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PI Bard JA, Walker MW, Branchek T, Weinshank RL;
XX WPI; 1995-246190/32.
XX P-PSDB; AAR79119.
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PT New nucleic acid encoding a Y4-Receptor, anti-sense mols. and ligands -
XX useful for treating amnesia, feeding/sleeping disorders or epilepsy, etc.
XX Claim 8; Fig 1; 154pp; English.
XX
CC The sequence encodes a human neuropeptide Y/peptide YY/pancreatic
CC polypeptide (Y4) receptor, which can be expressed from a vector adapted
CC for expression in a bacterial, mammalian, yeast or insect cell.
CC Specifically pcEXV-Y4 (ATCC 75631) and pcEXV-Y4 expression in COS-7,
CC LM(tk) - or NIH3T3 cells. The Y4 receptor can be used to screen drugs
CC which bind to it, specifically to find ligands (agonists or antagonists)
CC which bind to it. The ligands can be used to treat abnormalities.

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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6	1128	85.5	1128	4	AAI12802 Human neu
7	1128	85.5	1128	7	ABZ42706 Human neu
8	959.4	72.7	983	4	AAI23787 Probe #13
9	959.4	72.7	983	4	ABA35852 Probe #14
10	959.4	72.7	983	4	AAK43019 Human bon
11	811.2	61.5	1440	2	AAQ94172 Neuropept
12	807.8	61.2	1500	6	AAI72366 NPY4-R ge
13	278.6	21.1	2280	2	AAI36127 Mouse neu
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16	257.6	19.5	1152	3	AAK2588 Rhesus Y1
17	257.6	19.5	1152	3	AAK2587 Rhesus Y1
18	257.6	19.5	1155	9	AAK2586 Human neu
19	257.6	19.5	1605	4	AAI77580 Human neu
20	257.6	19.5	1605	4	AAI77580 Human neu
21	257.6	19.5	1605	5	AAI77580 Human neu
22	257.6	19.5	1605	5	AAI77580 Human neu
23	257.6	19.5	1605	6	ABN84250 Human neu

CC probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pat_sequences
XX Sequence 1959 BP; 402 A; 554 C; 494 G; 494 T; 0 U; 15 Other;

Query Match 91.7%; Score 1210; DB 4; Length 1959;
Best Local Similarity 96.9%; Pred. No. 8.8e-284;
Matches 1279; Conservative 0; Mismatches 34; Indels 7; Gaps 5;

QY 1 AGTATTGTTGTTCTGTTGCTGTAGGGCGTCATCCCTCAAGTGATCACTAGTTCAA 60
DB 88 AGTATTGTTGTTCTGTTGCTGTGTA-GGCGTCATCCCTCAAGTGATCACTAGTTCAA 146
QY 61 GAGTCCTGGAATCTTTTACATCACTATGAACACCTTCACCTCGCTGCTGCTC 120
DB 147 GAGTCCTGGAATCTTTTACATCACTATGAACACCTTCACCTCGCTGCTGCTC 206
QY 121 CCAAAATCTCCAGAGTGAAACAGAGCAACACCTCGGACCCCATACAACTTCTCT 180
DB 207 CCAAAATCTCCAGAGTGAAACAGAGCAACACCTCGGACCCCATACAACTTCTCT 266
QY 181 GAACATTCAGGATTCGCTGACGATGCTTCTTATCGTCACTTCTTACAGCATTGAG 240
DB 267 GAACATTCAGGATTCGCTGACGATGCTTCTTATCGTCACTTCTTACAGCATTGAG 326
QY 241 ACTGCTGGGGTCTGGGTGACCTGCTGATGCTGCTGATGCTGCTGAGGAGAGGAG 300
DB 327 ACTGCTGGGGTCTGGGTGACCTGCTGATGCTGCTGATGCTGCTGAGGAGAGGAG 386
QY 301 AAAGCCAACTGACCAACCTGCTTATCCCAACCTGGCCCTTCTGACTTCTCTCATGTGC 360
DB 387 AAAGCCAACTGACCAACCTGCTTATCCCAACCTGGCCCTTCTGACTTCTCTCATGTGC 446
QY 361 CTCCTCTGCAGCGCTGACCGCGCTCTACACCATCATGCACTACTGGATCTTTGAGAG 420
DB 447 CTNNNTTGCNAGCGGTGACCGCGCTCTACACCATCATGCACTACTGGATCTTTGAGAG 506
QY 421 ACCCTCTGCAAGATGTGGGCTTTCATCCAGTGATGCTGGTGACGGTCTCCATCTCTCG 480
DB 507 ACCCTCTGCAAGATGTGGGCTTTCATCCAGTGATGCTGGTGACGGTCTCCATCTCTCG 566
QY 481 CTCGCTCTGCTGGGCTGAGAGCATCAGCTCATCATCAACCAACAGGCTGGAAGCCC 540
DB 567 CTCGCTCTGCTGGGCTGAGAGCATCAGCTCATCATCAACCAACAGGCTGGAAGCCC 626
QY 541 AGCATCTCAGAGGCTACCTGGGATGCTCATCTGGGTGCTTGGCTGTGCTCTCTCC 600
DB 627 AGCATCTCAGAGGCTACCTGGGATGCTCATCTGGGTGCTTGGCTGTGCTCTCTCC 686
QY 601 CTGGCCTTCTGGGCAACAGCATCTGGAGATGCTTTCACAGAACCACTCCAGAGCT 660
DB 687 CTGGCCTTCTGGGCAACAGCATCTGGAGATGCTTTCACAGAACCACTCCAGAGCT 746
QY 661 CTGGAGTTCCTGGCAGATAGGTGCTGTACCCAGTCTGGCCACTGGCTCACCACCGC 720
DB 747 CTGGAGTTCCTGGCAGATAGGTGCTGTACCCAGTCTGGCCACTGGCTCACCACCGC 806
QY 721 ACCATCTACACCATCTCTCTCTCTTCCAGTACTGCTTCCCATCTGGGCTTCATCTG 780
DB 807 ACCATCTACACCATCTCTCTCTCTTTCAGTACTGCTTCCCATCTGGGCTTCATCTG 866
QY 781 GTCTGTTATGACCATCTACCGGCTCTGACAGAGGAGGGGCGCTGTTTCACAGGGC 840
DB 867 GTCTGTTATGACCATCTACCGGCTCTGACAGAGGAGGGGCGCTGTTTCACAGGGC 926
QY 841 ACCTACAGCTTCGAGCTGGGCAATGAGAGAGCTCAATGTGGTGTGCTGGTGTGATGGTG 900
DB 927 ACCTACAGCTTCGAGCTGGGCAATGAGAGAGCTCAATGTGGTGTGCTGGTGTGATGGTG 986

QY 901 GTGSCCTTTCGCGTCTGCTGCTGCTTCTCATGTGTTCAACAGCCTTGGAGACTGGCAC 960
DB 987 GTGSCCTTTCGCGTCTGCTGCTGCTTCTCATGTGTTCAACAGCCTTGGAGACTGGCAC 1046
QY 961 CATGAGCCATTCCTCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
DB 1047 CATGAGCCATTCCTCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1106
QY 1021 ATGSCCTTTCGCGTCTGCTGCTGCTTCTCATGTGTTCAACAGCCTTGGAGACTGGAG 1080
DB 1107 ATGSCCTTTCGCGTCTGCTGCTGCTTCTCATGTGTTCAACAGCCTTGGAGACTGGAG 1164
QY 1081 GAGATCAAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
DB 1165 GAGATCAAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1222
QY 1141 CTGSCCTTTCGCGTCTGCTGCTGCTTCTCATGTGTTCAACAGGCTTGGAGACTGGAG 1200
DB 1223 CTGSCCTTTCGCGTCTGCTGCTGCTTCTCATGTGTTCAACAGGCTTGGAGACTGGAG 1282
QY 1201 TCCATTCCTTTCGCGTCTGCTGCTGCTTCTCATGTGTTCAACAGGCTTGGAGACTGG 1260
DB 1283 TCCATTCCTTTCGCGTCTGCTGCTGCTTCTCATGTGTTCAACAGGCTTGGAGACTGG 1342
QY 1261 CACTTAGTCAAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
DB 1343 CACTTAGTCAAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1400
RESULT 4
AAK29996
ID AAK29996 standard; DNA; 1959 BP.
XX
AC AAK29996;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed single exon probe SEQ ID NO: 4553.
XX
KW Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
OS Homo sapiens.
XX
PN WO200157276-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000668.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488900/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.
XX
PS Example 4; SEQ ID NO 4553; 659pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers.

CC and genomic fragments and in research and diagnostic applications. The
CC array can detect changes in expression in a large number of genes coding
CC for different signaling pathway populations which can be used to diagnose
CC various diseases including cancer e.g. adenocarcinoma and leukaemia,
CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
CC and Parkinson's disease. The present sequence represents a polynucleotide
CC probe of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docID=0650093981
XX

SQ Sequence 1180 BP; 234 A; 382 C; 285 G; 279 T; 0 U; 0 Other;
Query Match 89.4%; Score 1180; DB 7; Length 1180;
Best Local Similarity 100.0%; Pred. No. 1.4e-276;
Matches 1180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 61 GAGTCTCGGAATCTTTTTCACATCCACATATGACACCTCTCACCTCTGCGCTTGTCTC 120
Db 1 GAGTCTCGGAATCTTTTTCACATCCACATATGACACCTCTCACCTCTGCGCTTGTCTC 60
Qy 121 CCAAAATCTCCACAGGTGAACAGAGCAAGCAAAACCCCTGGGCACCCCATACAACTTCTCT 180
Db 61 CCAAAATCTCCACAGGTGAACAGAGCAAGCAAAACCCCTGGGCACCCCATACAACTTCTCT 120
Qy 181 GAAATTCGCCAGGATTCCTGGAGCGTGAATGCTTTCATCTGCTTCTTCTTCTTCTTCTG 240
Db 121 GAAATTCGCCAGGATTCCTGGAGCGTGAATGCTTTCATCTGCTTCTTCTTCTTCTTCTG 180
Qy 241 ACTGTCTGGGGGCTCTGGGTAACTCTGCTCTGATGTGTGACTGTGAGCGCAGAGAGGAG 300
Db 181 ACTGTCTGGGGGCTCTGGGTAACTCTGCTCTGATGTGTGACTGTGAGCGCAGAGAGGAG 240
Qy 301 AAAGCCAAAGTGAACACCTCTTATGCGCAACCTGGCCCTTCTGACTTCTTCTTCTTCTG 360
Db 241 AAAGCCAAAGTGAACACCTCTTATGCGCAACCTGGCCCTTCTGACTTCTTCTTCTTCTG 300
Qy 361 CTCCTCTGCCAGCGCTGACCGCGTCTTACACCATCATGAGTACTGGATCTTTTGAGAG 420
Db 301 CTCCTCTGCCAGCGCTGACCGCGTCTTACACCATCATGAGTACTGGATCTTTTGAGAG 360
Qy 421 ACCCTCTGCAAGATGTGGCTTTCATCCAGTGCAATGCTGAGCGTCTTCTTCTTCTTCTG 480
Db 361 ACCCTCTGCAAGATGTGGCTTTCATCCAGTGCAATGCTGAGCGTCTTCTTCTTCTTCTG 420
Qy 481 CTCGTCTCTGGTGGCCCTGGAGGCGATCAGCTCATCATCAACCAACAGAGCTGGAAGCCC 540
Db 421 CTCGTCTCTGGTGGCCCTGGAGGCGATCAGCTCATCATCAACCAACAGAGCTGGAAGCCC 480
Qy 541 AGCATCTCACAGGCTTACCTGGGATTTGCTCATCTGCGTCAATGCTTGTCTTCTTCTTCC 600
Db 481 AGCATCTCACAGGCTTACCTGGGATTTGCTCATCTGCGTCAATGCTTGTCTTCTTCTTCC 540
Qy 601 CTGCGCTTCTGGCCCAACAGCATCTGAGAGATGTCTTCCACAGAGACCACTCCAGGCT 660
Db 541 CTGCGCTTCTGGCCCAACAGCATCTGAGAGATGTCTTCCACAGAGACCACTCCAGGCT 600
Qy 661 CTGAGATTCCTGGCAGATAAGGTGTCTGTATCCAGATCTCTGGCCACTGGCTCACACCGC 720
Db 601 CTGAGATTCCTGGCAGATAAGGTGTCTGTATCCAGATCTCTGGCCACTGGCTCACACCGC 660
Qy 721 ACCATCTACACACTTCTGCTTCTTCTTCCAGTACTGCTTCCACTGGGCTTATCTCTG 780
Db 661 ACCATCTACACACTTCTGCTTCTTCTTCCAGTACTGCTTCCACTGGGCTTATCTCTG 720
Qy 781 GTCGTGTATGACAGCATCTACCGGGCTCTGACAGAGCGAGGGCGGTGTTTTCACAGGGC 840
Db 721 GTCGTGTATGACAGCATCTACCGGGCTCTGACAGAGCGAGGGCGGTGTTTTCACAGGGC 780
Qy 841 ACCCTACAGTTCCGAGCTGGGACATGAGAGCGGTCAATGTGCTGCTGCTGGTGAATGTG 900
Db 781 ACCCTACAGTTCCGAGCTGGGACATGAGAGCGGTCAATGTGCTGCTGCTGGTGAATGTG 840

Qy 901 GTGGCCCTTGGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Db 841 GTGGCCCTTGGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Qy 961 CATGAGGCGATCCCATCTGCGACAGGAACTCATCTTCTTAGTGTGCTGCTGCTGCTG 1020
Db 901 CATGAGGCGATCCCATCTGCGACAGGAACTCATCTTCTTAGTGTGCTGCTGCTGCTG 960
Qy 1021 ATGGCTTCCACTGCTGCTCAACCCATTCATCTATGGCTTCTTCAACACCAACTTCAAGA 1080
Db 961 ATGGCTTCCACTGCTGCTCAACCCATTCATCTATGGCTTCTTCAACACCAACTTCAAGA 1020
Qy 1081 GAGATCAAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
Db 1021 GAGATCAAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
Qy 1141 CTGCCCCCTGTCCACAGTACATAGCGAAGTCTCCAAAGGCTCCCTGAGGCTAAGTGG 1200
Db 1081 CTGCCCCCTGTCCACAGTACATAGCGAAGTCTCCAAAGGCTCCCTGAGGCTAAGTGG 1140
Qy 1201 TCCAAATCCATTTAACACGCTTAGGCTTCTTCCCTTGCCA 1240
Db 1141 TCCAAATCCATTTAACACGCTTAGGCTTCTTCCCTTGCCA 1180

RESULT 6

AAD12802
ID AAD12802 standard; DNA; 1128 BP.
XX
AC AAD12802;
XX
DT 16-OCT-2001 (first entry)
XX
DE Human neuropeptide Y (NPY) Y4 receptor DNA.
XX
KW Human; neuropeptide Y; NPY; bone disease; bone mass; gene therapy;
KW cerebrospinal fluid; CSF; inositol phosphate; IP; Paget's disease;
KW fracture; extracellular signal-regulated kinase; ERK; osteoporosis;
KW osteopenia; bone metastasis; neurotransmitter; osteogenic;
KW NPY Y4 receptor; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 1. 1128
FT /*tag= a
FT /product= "Human neuropeptide Y (NPY) Y4 receptor"
XX
PN WO200153477-A1.

XX 26-JUL-2001.
XX 22-JAN-2001; 2001WO-US002040.
XX 20-JAN-2000; 2000US-00489872.
XX (BAYU) BAYLOR COLLEGE MEDICINE.
XX (AMLI/) AMLING M.
XX Amling M, Karsenty G, Ducey P;
XX WPI; 2001-488709/53.
XX P-PSDB; AA806691.
XX
XX Treating or preventing reduced bone mass, e.g. osteoporosis, by reducing
XX the level of neuropeptide Y activity in blood or cerebrospinal fluid.
XX
XX Example 7; Page 86; 102pp; English.
XX
XX The present invention relates to a method for treatment or prevention of
XX bone diseases characterised by loss of bone mass, comprises administering
XX to a mammal a compound that lowers the level of neuropeptide Y (NPY) in
XX the serum or cerebrospinal fluid (CSF) or a compound that lowers the

CC level of inositol phosphate (IP) or extracellular signal-regulated kinase
 CC (ERK). The method is specifically used to treat (including by gene
 CC therapy) or prevent osteoporosis, osteopenia or Paget's disease, but may
 CC also be used e.g., in cases of fractures or bone metastases. These
 CC diseases may also be diagnosed by detecting elevated NPY levels, in
 CC including monitoring of treatment, assessing efficacy of compounds in
 CC clinical trials and for identifying subjects at risk. The present
 CC sequence is a human NPY Y4 receptor DNA
 XX
 SQ

Query Match 85.5%; Score 1128; DB 4; Length 1128;
 Best Local Similarity 100.0%; Pred. No. 6.1e-264; Indels 0; Gaps 0;
 Matches 1128; Conservative 0; Mismatches 0;
 QY 88 ATGAACACCTCTCACTCTCTGCGCTTGTCTGCCAAATCTCCAAAGGTGAACACAGA 147
 DB 1 ATGAACACCTCTCACTCTCTGCGCTTGTCTGCCAAATCTCCAAAGGTGAACACAGA 60
 QY 148 AGCAACCCCTGGGACCCCATACACTCTCTGACATTCGCCAGGATTCGGTGCAGTG 207
 DB 61 AGCAACCCCTGGGACCCCATACACTCTCTGACATTCGCCAGGATTCGGTGCAGTG 120
 QY 208 ATGGTCTTCATCGTCACTCTCTACAGCATTCGAGACTGTCGGGGTCTCGGTAACTC 267
 DB 121 ATGGTCTTCATCGTCACTCTCTACAGCATTCGAGACTGTCGGGGTCTCGGTAACTC 180
 QY 268 TGCTGATGTGTGACTGTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 327
 DB 181 TGCTGATGTGTGACTGTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
 QY 328 GCCAACCCTGGCTCTCTCACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 387
 DB 241 GCCAACCCTGGCTCTCTCACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
 QY 388 TACACATCATGACTACTGAGTCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 447
 DB 301 TACACATCATGACTACTGAGTCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
 QY 448 CAGTGATCTGGTGAGGCTCTCCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 507
 DB 361 CAGTGATCTGGTGAGGCTCTCCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 QY 508 CAGCTCATCATCAACCCAGAGCTGGAAGCCAGCATCTCAGAGCCCTACCTGGGAT 567
 DB 421 CAGCTCATCATCAACCCAGAGCTGGAAGCCAGCATCTCAGAGCCCTACCTGGGAT 480
 QY 568 GTGCTCATCTGGTCACTTCCCTGTGCTCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 627
 DB 481 GTGCTCATCTGGTCACTTCCCTGTGCTCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
 QY 628 GAGATGTCTTCCCAAGAACCACTCCAGGCTCTGAGTCTCTGGCAGATAGGTGGTC 687
 DB 541 GAGATGTCTTCCCAAGAACCACTCCAGGCTCTGAGTCTCTGGCAGATAGGTGGTC 600
 QY 688 TGTACGAGTCTGGGCACTGGCTCACCACCGACCATCTACACACCTTCCTGCTCCTC 747
 DB 601 TGTACGAGTCTGGGCACTGGCTCACCACCGACCATCTACACACCTTCCTGCTCCTC 660
 QY 748 TTCAGTACTGCTCCCACTGGGCTTCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 807
 DB 661 TTCAGTACTGCTCCCACTGGGCTTCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
 QY 808 CTGACAGGAGGGGGCGGTGTTTCAAGAGGACCTACAGCTTGGAGCTGGGACATG 867
 DB 721 CTGACAGGAGGGGGCGGTGTTTCAAGAGGACCTACAGCTTGGAGCTGGGACATG 780
 QY 868 AAGCAGTCAATGT 927
 DB 781 AAGCAGTCAATGT 840
 QY 928 CTGCATGTGTCAACAGCTTGAAGACTGACCATGAGGCCATCCCATCTGCCACGGG 987

DB 841 CTGCATGTGTCAACAGCCTGGAAGACTGGACACCATGAGGCCATCCCATCTGCCACGG 900
 QY 988 AACCTCATCTTCTTAGTGTGCCACTTGTCTTGGCATGGCTCCACCTGCGCTCAACCCATT 1047
 DB 901 AACCTCATCTTCTTAGTGTGCCACTTGTCTTGGCATGGCTCCACCTGCGCTCAACCCATT 960
 QY 1048 ATCTATGGCTTCTCAACACCACTTCAAGAGGAGATCAAGGCCCTGTGCTGATTCG 1107
 DB 961 ATCTATGGCTTCTCAACACCACTTCAAGAGGAGATCAAGGCCCTGTGCTGATTCG 1020
 QY 1108 CAGCAGAGGCCCTCTGGAGGAGTGGAGACTCTGCCCTGTCCACAGTACATACGGAA 1167
 DB 1021 CAGCAGAGGCCCTCTGGAGGAGTGGAGACTCTGCCCTGTCCACAGTACATACGGAA 1080
 QY 1168 GTCTCCAAAGGGTCTCTGAGGCTAAGTGGCAGTCCCAATCCCAATTAA 1215
 DB 1081 GTCTCCAAAGGGTCTCTGAGGCTAAGTGGCAGTCCCAATCCCAATTAA 1128

RESULT 7

ABZ42706

ID ABZ42706 standard; DNA; 1128 BP.

XX AC

XX ABZ42706;

XX DT 04-MAR-2003 (first entry)

XX DE

XX Human neuropeptide Y receptor type 4 nucleotide SEQ ID NO:202.

XX KW

G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 G protein-coupled receptor modulator; antibody; immune-related disease;
 growth-related disease; cell regeneration-related disease; AIDS; cancer;
 immunological-related cell proliferative disease; autoimmune disease;
 Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 ulcer; gene; ds.

XX OS

XX Homo sapiens.

XX FN

XX WO200261087-A2.

XX PD

XX 08-AUG-2002.

XX PF

XX 19-DEC-2001; 2001WO-US050107.

XX XX

XX 19-DEC-2000; 2000US-0257144P.

XX PA

XX (LIFE-) LIFESPAN BIOSCIENCES INC.

XX PI

XX Burmer GC, Roush CL, Brown JP;

XX XX

XX WPI; 2003-046718/04.

XX DR

XX P-FSDS; ABP1859.

XX PT

New isolated antigenic peptides e.g., for G protein-coupled receptors
 (GPCR), useful for diagnosing and designing drugs for treating conditions
 in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
 autoimmune diseases.

XX PS

XX Disclosure; Fig 1; 523pp; English.

XX CC

The present invention describes antigenic peptides (I) comprising: (a)
 any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 acids. Also described: (1) an assay for the detection of a particular G
 protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 and (2) an isolated antibody having high specificity and high affinity or
 avidity for a particular GPCR. (I) can be used as GPCR modulators and in
 gene therapy. The antigenic peptides for GPCRs are useful in detecting an
 antibody against a particular GPCR, and in the production of specific

CC expression, the probes are therefore useful in grading and/or staging of
CC diseases of the cervix, notably cervical cancer. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 983 BP; 188 A; 300 C; 239 G; 242 T; 0 U; 14 Other;

Query Match 72.7%; Score 959.4; DB 4; Length 983;
Best Local Similarity 98.0%; Pred. No. 5.3e-223;
Matches 963; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 52 TTAGTTCAGAGTCTCTGGAAATCTTTTACATCCACTATGAACACCTCTCAGCTCTGGCC 111
DB 1 TTAGTTCAGAGTCTCTGGAAATCTTTTACATCCACTATGAACACCTCTCAGCTCTGGCC 60
QY 112 TTGCTGCTCCCAATCTCCACAGGTGAACAGCAAGCAACCCCTGGGACCCCATAC 171
DB 61 TTGCTGCTCCCAATCTCCACAGGTGAACAGCAAGCAACCCCTGGGACCCCATAC 120
QY 172 AACTTCTCTGAACATTGCCAGGATTCGGTGGACGTGATGGTCTTCATCGTCACTTCCTAC 231
DB 121 AACTTCTCTGAACATTGCCAGGATTCGGTGGACGTGATGGTCTTCATCGTCACTTCCTAC 180
QY 232 AGCATGAGACTGTCTGGGGGTCTCTGGGTACCTCTGCCTGATGTGTGACTGTGAGG 291
DB 181 AGCATGAGACTGTCTGGGGGTCTCTGGGTACCTCTGCCTGATGTGTGACTGTGAGG 240
QY 292 CAGAGGAGAAAGCAACCTGTGACCAACCTGCTTATCGCAACCTGGCCTTCTCTGACTTC 351
DB 241 CAGAGGAGAAAGCAACCTGTGACCAACCTGCTTATCGCAACCTGGCCTTCTCTGACTTC 300
QY 352 CTCATGTGCTCTCTGCGAGCGGTGACCGCGCTCTACACCATCATGACTACTGTGATC 411
DB 301 CTCATGTNNCTNNCTTGNACGCGGTGACCGCGCTCTACACCATCATGACTACTGTGATC 360
QY 412 TTGAGAGACCTCTGCAAGATGTGCGCTTCATCCAGTGTGATCGGTGAGGTCTCC 471
DB 361 TTGAGAGACCTCTGCAAGATGTGCGCTTCATCCAGTGTGATCGGTGAGGTCTCC 420
QY 472 ATCTCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 531
DB 421 ATCTCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 532 TCGAAGCCAGCATCTCAGAGCCCTACTCTGGGATGTGCTCATCTGGTCTATGCTGCTGT 591
DB 481 TCGAAGCCAGCATCTCAGAGCCCTACTCTGGGATGTGCTCATCTGGTCTATGCTGCTGT 540
QY 592 GTCTCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 651
DB 541 GTCTCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 652 TCGAAGCCAGCATCTCAGAGCCCTACTCTGGGATGTGCTCATCTGGTCTATGCTGCTGT 711
DB 601 TCGAAGCCAGCATCTCAGAGCCCTACTCTGGGATGTGCTCATCTGGTCTATGCTGCTGT 660
QY 712 CACCAAGCCAGCATCTCAGAGCCCTACTCTGGGATGTGCTCATCTGGTCTATGCTGCTGT 771
DB 661 CACCAAGCCAGCATCTCAGAGCCCTACTCTGGGATGTGCTCATCTGGTCTATGCTGCTGT 720
QY 772 TTCATCTGCTGTGTATGCAAGATGTACCGGCGCTGCTGAGAGCGAGGCGGTGTGT 831
DB 721 TTCATCTGCTGTGTATGCAAGATGTACCGGCGCTGCTGAGAGCGAGGCGGTGTGT 780
QY 832 CACAGGGCAGCTCAGAGTCTGGAGTGGGACATGAGAGGAGTCAATGTGCTGCTGTG 891
DB 781 CACAGGGCAGCTCAGAGTGGAGTGGGACATGAGAGGAGTCAATGTGCTGCTGTG 840
QY 892 GTGATGGTGGTGGTCTTGGCGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 951
DB 841 GTGATGGTGGTGGTCTTGGCGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
QY 952 GACTGGCAGCATGAGGCGCATCCCATCTGCTGCCACGGGACCTCATCTTCTTAGTGTGCCAC 1011

DB 901 GACTGGCAGCATGAGGCGCATCCCATCTGCCATGGGAGCACTCATCTTCTTAGTGTGCCAC 960
QY 1012 TTGCTTGGCATGGCTTCCACCTG 1034
DB 961 TTGCTTGGCATGGCTTCCACCTG 983
RESULT 9
ABA35852
ID ABA35852 standard; DNA; 983 BP.
XX ABA35852;
XX AC
XX DT 23-JAN-2002 (first entry)
XX DE Probe #14318 for gene expression analysis in human heart cell sample.
XX KW Human; gene expression; heart; microarray; vascular system; probe;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease; ss.
XX OS Homo sapiens.
XX PN WO200157274-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000666.
XX PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488899/53.
XX PS Single exon nucleic acid probes for analyzing gene expression in human hearts.
XX Claim 4; SEQ ID NO 14318; 530pp; English.
CC The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 983 BP; 188 A; 300 C; 239 G; 242 T; 0 U; 14 Other;
Query Match 72.7%; Score 959.4; DB 4; Length 983;
Best Local Similarity 98.0%; Pred. No. 5.3e-223;
Matches 963; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 52 TTAGTTCAGAGTCTCTGGAAATCTTTTACATCCACTATGAACACCTCTCAGCTCTGGCC 111
DB 1 TTAGTTCAGAGTCTCTGGAAATCTTTTACATCCACTATGAACACCTCTCAGCTCTGGCC 60
QY 112 TTGCTGCTCCCAATCTCCACAGGTGAACAGCAAGCAACCCCTGGGACCCCATAC 171

882 GCGTATCTATCAGCGCTGTCAGAGGCGAGGGCGTGGTTCCACAGCACACTTGCAGCTC 941
852 GCGAGCTGGGCAATGAGAGAGTCAATGCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGG 911
942 ACAGTGGGCGAGTGAAGCGGATCAATGCGATGCTCATGGCAATGCTCACTGGCTTGC 1001
912 CCGTCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 971
1002 AGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1061
972 CCCATCTGCGAGGGAACCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1031
1062 CCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1121
1032 CTGGCTCAACCCATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1091
1122 CTGCTCAACCCCTTCT 1181
1092 CCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1151
1182 TCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1241
1152 CACAGTACATCAGGAGCTCTCCAAAGGCTCCCTGAGGCTAAGTGGAGTCCCAATCCAT 1211
1242 CACTGTGCACAGGACCTCTCCAAAGGATCTATGAGGATGGTAGGAGTCAAGTCACT 1301
1212 TTAACCAAGGCTAGGCT 1271
1302 GTAGTCATGCTAGG--CTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1359
1272 GTGGGCACTGCAAGTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG 1317
1360 GTAGACACAATGCAAGTGGTGTATCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1405

RESULT 12

AA172366
ID AA172366 standard; DNA; 1500 BP.
AC AA172366;
DT 15-MAY-2002 (first entry)
DE NPY4-R gene.

Gene, non-human; transgenic; mouse; G protein-coupled receptor; GPCR;
gene therapy; neurological disease; neuropsychological disease; KDR3;
psychotic illness; DEZ receptor; CB2R; adrenomedullin receptor; CRFR2;
corticotropin-releasing factor receptor; neuropeptide Y receptor gene;
N-formylpeptide receptor-like 3; PPRL3; NPY6-R; kappa-3 opiate receptor;
metabotropic glutamate receptor; mGluR8; MAS receptor; NPY4-R;
targeting arm; ds.
Mus musculus.

Key Location/Qualifiers
FH misc_difference 339..440
FT /*tag= a
FT /*note= "Deleted in targeting construct"

WO200203789-A2.
17-JAN-2002.
06-JUL-2001; 2001WO-US021498.
06-JUL-2000; 2000US-0216108P.
06-JUL-2000; 2000US-0216250P.
06-JUL-2000; 2000US-0216252P.
06-JUL-2000; 2000US-0216253P.
06-JUL-2000; 2000US-0216254P.
06-JUL-2000; 2000US-0216259P.
06-JUL-2000; 2000US-0216260P.

06-JUL-2000; 2000US-0216271P.
06-JUL-2000; 2000US-0216473P.
06-JUL-2000; 2000US-0216475P.
19-JUL-2000; 2000US-0219403P.
27-JUL-2000; 2000US-0221473P.
27-JUL-2000; 2000US-0221474P.
27-JUL-2000; 2000US-0221484P.
27-JUL-2000; 2000US-0221490P.
27-JUL-2000; 2000US-0221497P.
07-AUG-2000; 2000US-0223625P.
06-DEC-2000; 2000US-0251815P.
16-JAN-2001; 2001US-0262137P.
16-JAN-2001; 2001US-0262138P.
29-MAR-2001; 2001US-0280264P.
26-JUN-2001; 2001US-0300929P.
(DELT-) DELTAGEN INC.
XX Allen KD, Brennan TJ;
XX WPI; 2002-154854/20.
XX Novel non-human transgenic animal, preferably transgenic mice comprising
PT disruptions in target G protein-coupled receptor gene, useful for
PT identifying an agent that modulates expression or function of target
PT gene.

Example 6; Fig 16; 93pp; English.

This sequence represents the neuropeptide Y receptor gene (NPY4-R). The
targeting arms (AA172367-68) were used to disrupt this gene. The
resulting sequence was used in the production of a non-human transgenic
animal, preferably a mouse, with targeted G protein-coupled receptor gene
disruption in the NPY4-R gene. The transgenic animal is useful for
identifying an agent that modulates the expression or function of the
target gene, by administering an agent, and determining whether the
expression or function of the target is modulated. It is also useful for
testing the efficacy of proposed genetic and pharmacological therapies
for human genetic diseases, such as neurological, neuropsychological or
psychotic illnesses. The transgenic mice are useful as models for
diseases, disorders or conditions associated with phenotypes relating to
a disruption in a target, and to identify drugs, pharmaceuticals, disease
therapies and interventions which may be effective in treating a disease
or other phenotypic characteristics of the animal

Sequence 1500 BP; 320 A; 428 C; 312 G; 440 T; 0 U; 0 Other;

Query Match 61.2%; Score 807.8; DB 6; Length 1500;
Best Local Similarity 76.5%; Pred. No. 4.1e-186;
Matches 1003; Conservative 0; Mismatches 307; Indels 1; Gaps 1;

QY 7 GTTGTCTGTTGGCTTTAGGGCGTTCATCCCTCAAGTGTATCACTTAGTTCAGAGTCC 66
DB 123 GTTCCATTGTTGTTTTCAGGCTGCATCTCTGAAGTAGGCCCTTTACTCTGGAGTTC 182
QY 67 TGGATCTTTTCACTATCCACTATGAACACCTCTCACTCTGGCTTGTCTGCCAAA 126
DB 183 CCGGATCTTTCACACCTACCATGAATACCTCTCATTTCTTGGCCCTCTCTTCCAGGA 242
QY 127 TCTCCACAAGGTGAAAACAGAAAGCAACCCCTGGGCGACCCCATACAACCTCTCTGAACAT 186
DB 243 TCCTACAGGTAAGNATGGGACCATCCATTGGATTCCCCCTATATTTCTCTGATGC 302
QY 187 TGCCAGGATTCGGTGACCGTGTATGGTCTTTCATCTGTCACCTCTACAGCATTTAGACTGTC 246
DB 303 TGCCAGGATTCGGGACGAACTGTTGGCTTTCATCATCCACCATCAGCATTTAGACCATC 362
QY 247 GTGGGGTCTCTGGTAACCTCTGCTGATGTGTGACTGTGCTGAGGAGAGAGAGAGCC 306
DB 363 TTAGGGGTCTCTGGAAACCTCTGCTTGATTTTGTGACACAGACAAAGAGAAAGTCC 422
QY 307 AACGTGACCAACCTGTTATGCCCACCTGGGCTTCTCTGACTTCTCTATGTGCTCTC 366

Db 423 AATGTGACCAACTACTCAATGTCACCACTGGCGTTCTCTGACTTCTCATGTGCGCTCATC 482
Qy 367 TCCAGCCGCTGACCGCCGCTTACACCATCATGAGTACTGTGATCTTTGGAGACCCCTC 426
Db 483 TGCACCACTACTCAGTACCTACCATCATGAGTACTGTGATCTTTGGTGAAGCTCCTT 542
Qy 427 TGCAGATGTCGGCCTTTCATCAGTGCATGTCGGTGACGCTCTCCATCTCTCGTCTGTC 486
Db 543 TGCAGATGTTAACTTTCATCAGTGTATGTGAGTGACAGTCTCCATCTCTCATCTGTC 602
Qy 487 CTCGTGCGCCTGAGAGGATCAGCTCATCATCAACCCCAAGGCTGGAAGCCCAAGCATC 546
Db 603 CTGTGCGCCTGAGAGACACCACTCATATCAATCCAAAGGCTGGAAGCCCAAGTATT 662
Qy 547 TCAAGCCCTACTGCGGATGTCATCATCTGGGTCATGCTGCTGCTGCTCTCTCTGCTGCC 606
Db 663 TTCCAGGCTACTCTGGGATGTCGTCATCTGGTTCATCTCTGTTTCTCTCTCTCTGCGG 722
Qy 607 TTCTGCGCAACAGACATCTCTGAGATGTCCTCCCAAGAACCACTTCCAAAGGCTCTGGAG 666
Db 723 TTCTGCGCAACAGACATCTGATGACCTTCTCCACTACACCACTCTAAGGTTGAGAG 782
Qy 667 TTCTGCGCAGTAAGTGTCTGTACCGAGTCTCTGCGCACTGCTGCTCACCACCGACCATC 726
Db 783 TTCTGCGAAGACAAGTCTCTCTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 842
Qy 727 TACACCACTTCT 786
Db 843 TATACCACTTCT 902
Qy 787 TATGCAAGCATATACCGCGCTGTCAGAGGAGGCGCGGTGTTTCAAGGGCACTTAC 846
Db 903 TACATACGATCTTACCAAGCGCTGTCAGAGGAGGAGGATGTTTCCATCGCACGCTTGC 962
Qy 847 AGCTTGGAGTGGGACATGAAGAGGTCATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 906
Db 963 AGCTTCAAGCGGGGAGATGAAGCGGATCAACAGATGCTCATGACATGCTGCTGCTGCC 1022
Qy 907 TTTCGCTGCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 966
Db 1023 TTTCGAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1082
Qy 967 GCATCCCATCTGCCAGGAGACCTCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1026
Db 1083 GCATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1142
Qy 1027 TCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1086
Db 1143 TCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1202
Qy 1087 AAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1146
Db 1203 AAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1262
Qy 1147 CTGTCACAGTATACATGGAAGTCTCCAAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1206
Db 1263 CTGTCACGCTTTCACAGGACCTCTCCAGGATCGATGAGGATGGTAGAAGTCTTAC 1322
Qy 1207 CCATTTACAGGCTTAGGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1266
Db 1323 TCCATATAGTGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1381
Qy 1267 GCTAAGTGGGCACATGCAAGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1317
Db 1382 GTTAAAGACATGTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1432

RESULT 13

AAT36127

ID AAT36127 standard; DNA: 2280 BP.

XX AC

AC AAT36127;

XX

25-OCT-1996 (first entry)
Mouse neuropeptide Y Yx receptor DNA.
Neuropeptide Y Yx receptor; NPY Yx; G-protein coupled receptor; obesity;
diabetes; cardiac vasospasm; Parkinson's disease; ds.
Mus sp.
Key Location/Qualifiers
CDS 822..1937
/*tag= a
W09623809-A1.
08-AUG-1996.
30-JAN-1996; 96WO-US001444.
03-FEB-1995; 95US-00383746.
03-APR-1995; 95US-00415818.
(MERI) MERCK & CO INC.
Cascieri MA, Linemeyer DL, Macneil DU, Shiao L, Strader C;
Weinberg DH, Tan CP;
WPI; 1996-371369/37.
P-PSDB; AAW02099.
DNA mol. encoding neuro-peptide Y Yx receptor - useful in assays to
identify cpds. which bind to receptor, useful to treat, e.g. obesity,
diabetes, cardiac vasospasm and Parkinson's disease.
Claim 1; Page 46-49; 65pp; English.
A PetI fragment (AAT36127) of pVE2841 codes for mouse neuropeptide Y
subtype Yx (NPY Yx) receptor (AAW02099). It was obtd. from a mouse cosmid
library using a probe generated by PCR amplification (see also AAT36131-
32) of NPY Y1 receptor cDNA. Vectors were constructed to allow expression
of the murine NPY Yx receptor DNA in mammalian (COS-7) cells. The
recombinant receptor, or transformed host cells, can be used to screen
for cpds. that modulate the function of the receptor, or modulate the
expression of nucleic acids encoding the receptor. Such cpds. are useful
for treating a variety of disease conditions
Sequence 2280 BP; 695 A; 466 C; 460 G; 659 T; 0 U; 0 Other;
Query Match 21.1%; Score 278.6; DB 2; Length 2280;
Best Local Similarity 53.2%; Pred. No. 1.8e-57;
Matches 637; Conservative 0; Mismatches 554; Indels 6; Gaps 2;
Qy 24 GTAGGCGCTCATCCCTCAAGTGATATCATCTTAGTTCAAGAGTCTCTGGAACTTTTCATC 83
Db 740 GTTCTCCTCTCAAGAACCAATGGCCAAACATCCACTGAGGATACACGGAAGCTTAGAAAT 799
Qy 84 CACTATGAACACCTCTCACCTCTCTGGCTTGTCTGCCAAATCTCCAAAGTGAAAA 143
Db 800 CTCATTAATTAATCTCTGACATATGGAAGTCTCACAAACAGCCACACCTATATAAC 859
Qy 144 CAGAAGCAAAACCCCTGGGCAACCCCATACAACTTCTCTGAACATTCGAGGATCCGTTGA 203
Db 860 CAGTGGCAAGAGCAACAACTCGGCATTTTCTACTTTTGAATCTCTGCCAACCCCTTTTCT 919
Qy 204 CGTGTGCTCTTCATCTCATCTTCTCTACAGCATTTGAGACTGTCTGGGGTCTGGGTAA 263
Db 920 AGCCATCTCTTGTCTACTCATAGCATATCTGTGATCTTAATCATGGCATTTTGGAAA 979
Qy 264 CCTCTGCTGTATGTGTGTGATGTGTGAGCGAGAGAGAGAGCC---AACGTGACCAACT 320
Db 980 CCTCTCTCTTATCATCATCTCTTTAAGAAACAGAGAGAGAGCTCAAAATGTTTACCAACAT 1039
Qy 321 GCTTATCGCCAACTGGCGCTTCTCTGACTTCTCTCATGTGCTCTCTCTGCGACCGCTGAC 380

Ddb 1761 AAATCCTCTCTTTTATGGGATTTCTCAACAAAACCTTCAGGAAGGATCTTAATGATGCTTAT 182
 Qy 1098 GGTGACTTGCCACGACGAGCGCCCCCTCGAGGAGTCGAGGCATCTGCCCTGTGCCACAGT 1157
 Ddb 1821 TCACCACCTGTGTGTGGTGAACCTCAGGAAGATTATGAATAATTGCCATGTCTACTAT 1880
 Qy 1158 ACATAGCGAAGTCTCCAAAGGTCCTGAGGCTAAGTGGCGAGTCCAATCCCATTTA 1214
 Ddb 1881 GCACACAGATGAATCCAAAGGATCATTTAAACTGGCTCACATACCACAGGCATATA 1937

RESULT 15
AAT36128
 ID AAT36128 standard; cDNA; 1499 BP.
 XX AC
 XX ATAT36128;
 XX 25-OCT-1996 (first entry)
 DE Human neuro peptide Y Yx receptor cDNA.
 XX Neuro peptide Y Yx receptor; NPY Yx; G-protein coupled receptor; obesity;
 KW diabetes; cardiac vasospasm; Parkinson's disease; ds.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FT CDS 182..1294
 FT /*tag= a
 XX W09623809-Al.
 XX 08-AUG-1996.
 XX 30-JAN-1996; 96WO-US001444.
 PR 03-FEB-1995; 95US-00383746.
 PR 03-APR-1995; 95US-00415818.
 PA (MERI) MERCK & CO INC.
 XX Cascieri WA, Linemeyer DL, Macneil DJ, Shiao L, Strader C;
 PI Weinberg DH, Tan CP;
 DR WPI: 1996-371369/37.
 DR P-PSDB; AA02100.
 PT DNA mol. encoding neuro.peptide Y Yx receptor - useful in assays to
 PT identify cpds. which bind to receptor, useful to treat, e.g. obesity,
 PT diabetes, cardiac vasospasm and Parkinson's disease.
 XX Claim 36; Page 53-54; 65pp; English.
 CC A cDNA clone (AAT36128) codes for human neuro peptide Y subtype Yx (NPY
 CC Yx) receptor (AAW02100). It was obtd. from a human heart cDNA library
 CC using a probe obcd. by PCR amplification of human genomic DNA using
 CC primers (see also AAT36135-36) based on the mouse NPY Yx receptor
 CC (AAT36127). Vectors were constructed to allow expression of the human NPY
 CC Yx receptor DNA in mammalian (COS-7) cells. The recombinant receptor, or
 CC transformed host cells, can be used to screen for cpds. that modulate the
 CC function of the receptor, or modulate the expression of nucleic acids
 CC encoding the receptor. Such cpds. are useful for treating a variety of
 CC disease conditions
 XX Sequence 1499 BP; 399 A; 400 C; 279 G; 421 T; 0 U; 0 Other;
 SQ Query Match 20.2%; Score 266; DB 2; Length 1499;
 Best Local Similarity 53.9%; Pred. No. 1.8e-54;
 Matches 592; Conservative 0; Mismatches 500; Indels 6; Gaps 2

Qy 75 TTTCATCATCATATGACACCTCTCACTCTCGCTTGTCTCTCCCAAATCTCCACA 134
 Db 151 TTAGAANAATCTCTTTCAATCTCTTGACACAAATGGAAGTTTCTTAACACCCAGCATC 210

Search completed: May 10, 2004, 22:22:49
Job time : 591 secs

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135 AGGTGAAACAGAAAGCAAAACCCCTGGGCACCCCATACAACTTCTCTGAACATGCGCAGA 194
194
211 TAATAACAACAGACACAAAGAACAACTCGGCAATTTTTTTTACTTTAGTCTCTGCAACC 270
270
195 TTCCGTGGAGGTGATGGTCTTCACTGCTCACTTCTTACAGCATTTAGACTGTCTGGGGGT 254
254
271 CCCTTCTCCAGCTTTACTCTCTATATATGCACTAGCTATCTGTGGTCTTAATTTGGGGCT 330
330
255 CTTGGGTAACTCTGCTGATGTGTGACTGTGAGCGAGAAAGGAGAAAGC---CAAGCT 311
311
331 TTTTGGAAACCTCTCTCATCATCATCTTTAAGAAAGCAGAGAGAAAGCTCAGAAATTT 390
390
312 GACCAAGCTCTTATGCGCAACCTGGCTTCTCTGACTTCTTCACTGCTCTCTCTGCGCA 371
371
391 CACCAGCATACTGATTTGCCAATCTCTCCCTCTCTGATACCTTGGTGTGTGATGGCAT 450
450
372 GCGCTGACCGCGTCTTACACCATCATGGACTACTGGATCTTTGGAGAGACCTCTTGCAA 431
431
451 CCAATTTACTATCATCTACACTCTGATGGACCACTGGATATTTGGGATACCATGTGCAG 510
510
432 GATGTGGCGCTTCAATCCAGTGCATGTGGTGAAGGCTCTCCATCTCTGCTGCTGCTCGT 491
491
511 ACTCACATCTATGTGCAGAGTGTCTCAATCTCTGTGTCCATATCTCACTTGTATTAC 570
570
492 GCGCTGGAGGCGCATCAGCTCATCATCAACCAACAGGCTGGAAGCCAGCATCTCACA 551
551
571 TGCTGTCGAAGATATCAGCTAATGTGAACCCCGTGGCTGGAGCCAGTGTGACTCA 630
630
552 GGCCTACTCTGGGATTTGTCTCATCTGGGTCAATGCTGTGCTCTCTCCCTGCGCTTCT 611
611
631 TGCCTACTGGGGCATCACATGATTTGGCTGTTTTCCCTTCTGCTGTCTATTCCCTTCT 690
690
612 GGCCAAACAGCATCTGGAGATGCTTCCACAGAACCACTCCAAAGGCTCTGGAGTTCT 671
671
691 CCTGTCTTACCACTCTACTGATGAGCCCTTCCACAACTCTCTCTCCGCTGACCTCA 750
750
672 GCGAGATAAGGTGTCTGTACCGAGTCTGTGCGCACTGGCTCACACCGCACCACTTACAC 731
731
751 CACCACCAAGGTGGCTGTGTGGAGAACTGGCCCTCCAAAAGGACCGGCTGCTCTTTCAC 810
810
732 CACCTTCTGCTCTCTCTCAGTACTGCTCCCACTGGGCTTCACTCTGCTGCTGTTATGC 791
791
811 CACCTCCCTTTTCTGTGTCAGTATTTGTCTCTAGGCTTCACTCTCACTGCTACTT 870
870
792 ACGCATCTACGGCGCTCTCAGAGCGAGGGCGGCTGTTTCAAGGGCACCTTACAGCTT 851
851
871 GAAGATTGTTATCTGCTCTCCGAGGAGAAATGCAAGGTAGATAAGAAAGGAGAAATGA 930
930
852 G---CGAGCTGGGACATGAAGCAGGTCAATGTGGTCTGTGGTGTGGTGGGCTT 908
908
931 GGGCCGGCTCAATGAGAAACAAGAGGATCAACAAATGTTGATTTCCATCGGTGGACCTT 990
990
909 TGCCGTGCTCTGCTGCTCTCTGATGTGTTCAACAGCCTGGAAGACTGGCACCATGAGGC 968
968
991 TGGAGCTGCTGGCTGCCCCCGAATATCTTCAATGTCTATCTTTGACTGGTATCATGAGT 1050
1050
969 CATCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGTGGCCATGGCCTC 1028
1028
1051 GCTGATGAGCTGCCACCGACCTGGTATTTGTAGTTTGGCCACTGGTGTGTATGGTTTC 1110
1110
1029 CACCTTGGTCAACCATTCATCTATGGCTTTCTCAACACCACTTCAAGAAAGGAGATCAA 1088
1088
1111 CACATGATAAACCCTCTCTTTATGGCTTCTCAACAAATTTCCAAAAGGACCTGGT 1170
1170
1089 GGCCTGTGTGTGATTTGCCACAGAGCGCCCTCTGGAGAGTCGGAGCATCTGCCCTT 1148
1148
1171 AGTGTCTTATTCACCACTGTGTGTGCTTCACTCAGGAAAGATGTGAAATATTTGCCAT 1230
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1149 GTCCACAGTACATACGGA 1166
1166
1231 CTCCACTATGCACACAGA 1248
1248
```

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 11, 2004, 10:52:27 ; Search time 3773 Seconds
(without alignments)
10447.410 Million cell updates/sec

Title: US-09-430-775-1

Perfect score: 1320

Sequence: 1 AGTATTGTTGCTGTTGC.....CCAGCATTCTCGGCTTCTG 1320

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: em_estba.*

2: em_esthum.*

3: em_estin.*

4: em_estmu.*

5: em_estov.*

6: em_estpl.*

7: em_estro.*

8: em_estc.*

9: gb_estl.*

10: gb_est2.*

11: gb_est3.*

12: gb_est4.*

13: gb_est5.*

14: gb_est5.*

15: em_estfun.*

16: em_estom.*

17: em_gss_hum.*

18: em_gss_inv.*

19: em_gss_pin.*

20: em_gss_vit.*

21: em_gss_fun.*

22: em_gss_mam.*

23: em_gss_mus.*

24: em_gss_pro.*

25: em_gss_rod.*

26: em_gss_pbg.*

27: em_gss_vrl.*

28: gb_gss1.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	797.6	60.4	3628	11 AK035505	AK035505 Mus muscu
2	396.6	30.0	426	12 BG875680	BG875680 MR2-CN003
3	371.2	28.1	602	10 BF040649	BF040649 BP250021A
4	371.2	28.1	642	10 BF041396	BF041396 BP250008B

C	5	363.8	27.6	453	13	BQ319790	BQ319790 CM0-CT081
C	6	342.8	26.0	406	10	AW378515	AW378515 QV4-HT022
	7	303	23.0	1149	29	AY413582	AY413582 Mus muscu
	8	287.6	21.8	679	13	BY733731	BY733731 BY733731
	9	278.6	21.1	2570	11	AK030279	AK030279 Mus muscu
	10	257.6	19.5	1155	29	AY413580	AY413580 Homo sapi
	11	254.2	19.3	639	10	BG628025	BG628025 BB638025
	12	252.4	19.1	1152	29	AY413581	AY413581 Pan trogl
	13	185.8	14.1	936	13	BU840743	BU840743 AGENCOURT
	14	159.8	12.1	669	13	BX506438	BX506438 DKF7779B
	15	156	11.8	1113	29	AY420480	AY420480 Homo sapi
	16	150.4	11.4	820	12	BI837108	BI837108 603090071
	17	150.2	11.4	1100	29	AY420481	AY420481 Pan trogl
	18	147.2	11.2	1113	29	AY420482	AY420482 Mus muscu
	19	142.2	10.8	621	9	AI790953	AI790953 uk49A05.Y
	20	138.8	10.5	1146	29	AY400451	AY400451 Mus muscu
	21	138.8	10.5	3335	11	AK049892	AK049892 Mus muscu
	22	138.2	10.5	1290	29	AY411591	AY411591 Homo sapi
	23	134.8	10.2	1296	29	AY411593	AK018543 Mus muscu
	24	130	9.8	3336	11	AK018543	AQ383893 RPI-11-13
C	25	129	9.8	459	28	AQ383893	AY400449 Homo sapi
	26	126.6	9.6	1146	29	AY400449	AI908179 IL-BT164-
	27	126.4	9.6	524	9	AI908179	AL837015 AL837015
	28	126.2	9.6	381	9	AL837015	AL258742 Tetraodon
	29	116.4	8.8	1070	29	CNS033N1	BM926262 AGENCOURT
	30	115.6	8.8	1245	12	BM926262	AW105870 u194h11.Y
	31	113.4	8.6	624	9	AW105870	AZ884183 RPI-23-1
	32	110.2	8.3	632	28	AZ884183	AY409053 Homo sapi
	33	109.4	8.3	1168	29	AY409053	AQ879138 HS_3184.B
	34	107.4	8.1	737	28	AQ879138	AK081276 Mus muscu
	35	104	7.9	2199	11	AK081276	AK035356 Mus muscu
	36	100.4	7.6	2121	11	AK035356	AL917309 AL917309
	37	95.8	7.3	539	9	AL917309	AY400450 Pan trogl
	38	93	7.0	833	29	AY400450	AZ237363 RPI-23-8
C	39	92.2	7.0	405	28	AZ237363	AK033443 Mus muscu
	40	89.4	6.8	1941	11	AK033443	AL528009 AL528009
	41	89	6.7	835	9	AL528009	F24590 HSPD11017.H
C	42	88.2	6.7	303	14	F24590	BC033742 Homo sapi
	43	87.6	6.6	2090	11	BC033742	CD559554 AGENCOURT
	44	87	6.6	762	14	CD559554	CD559553 AGENCOURT
	45	87	6.6	772	14	CD559553	

ALIGNMENTS

RESULT 1
AK035505
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

AK035505 3628 bp mRNA linear HTC 19-SEP-2003
Mus musculus adult male urinary bladder cDNA, RIKEN full-length
enriched library, clone:9530057L11 product:NEUROPEPTIDE Y RECEPTOR
TYPE 4, full insert sequence.

AK035505 1 GI:26330703

HTC; CAP trapper.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

99279253

PUBMED

10349636

2

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itch, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

20499374

PUBMED

11042159

Funding for cattle EST sequencing was provided by the USDA National Research Initiative, Animal Genome Resource Grant AG 99-3205-8534 to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED from Washington University Genome Center. Vector Trimmi 9: Cross match from Washington University Genome Center PHRAP suite. This sequence is vector free and at least 200 bp in length.

PCR Primers

FORWARD: TAATACGACTCACTATAGGG

BACKWARD: ATTAACCTCTACTTAAG

Insert Length: 602 Std Error: 0.00

Plate: BP250021A10 row: G column: 12

Seq primer: AGCGATAACAATTTCACACAGGA

High quality sequence stop: 602.

FEATURES

Location/Qualifiers

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/db_xref="taxon:9913"

/clone="BP250021A10G12"

/sex="female"

/lab_host="DH10B"

/note="Organ: placenta; Vector: pT73Pac; Site 1: EcoRI;

Site 2: NotI; The cDNA library was contributed by the

Soares laboratory and it was constructed and normalized

as described by Bonaldo, M.F., Lennon, G. and Soares,

M.B. (1996), Genome Research 6(9): 791-806."

ORIGIN

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Best Local Similarity 87.5%; Pred. No. 6.7e-68;

Mismatches 58; Indels 0; Gaps 0;

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Db 13 CTCTGTAGCTCCATACAACTTCTGACCACTGCCAGGATTCGTAGACCCCTGTCT 72

QY 215 TCATCGTCACTTCTACAGCAATTGAGACTGTCGGGGGCTCTGGTAACTCTGCTGA 274

Db 73 TCATGTCACTTCTACAGCAATTGAGCAATGTGGGTGCTCTGGCAACCTCTGCTGA 132

QY 275 TGTGTGACTGTGAGGAGAGGAGAAAGCCACGTCGACCAACTCTCTATCGCCAAAC 334

Db 133 TATGTGTGACTATTAGGCAGAGAGAGGCAATGTGACCAACTCTCTATTGCCAAC 192

QY 335 TGGCTTCTGACTTCTCTGCTCTCTGCTCTCTGCTCTCTGCTCTCTGCTCTCTG 394

Db 193 TGGCTTCTGACTTCTCTGCTCTCTGCTCTCTGCTCTCTGCTCTCTGCTCTCTG 252

QY 395 TCATGGACTCTGATCTTTGGAGAGACCCCTCTCAAGATGTGCGCTTCTATCCAGTGA 454

Db 253 TCATGGACTCTGATCTTTGGAGAGACCCCTCTCAAGATGTGCGCTTCTATCCAGTGA 312

QY 455 TGTGGTGAAGGCTCCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 514

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QY 515 TCATCAACCCCAAGGCTGAGGAGCCAGCACTCTCAAGGCTCTCTGAGGATTTGCTCA 574

Db 373 TCACCAATCCCAAGGCTGAGGAGCCAGCACTCTCAAGGCTCTCTGAGGATTTGCTCA 432

QY 575 TCTGGGTCAATGCTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 618

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RESULT 4

BF041396

LOCUS

DEFINITION

ACCESSION

VERSION

BF041396 642 bp mRNA linear EST 10-OCT-2000

BP250008B10E9 Soares normalized bovine placenta Bos taurus cDNA

clone BP250008B10E9 5', mRNA sequence.

BF041396

BF041396.1 GI:10758451

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

EST.

Bos taurus (cow)

Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Bovidae; Bovinae; Bos.

1 (bases 1 to 642)

Lewin, H.A., Soares, M.B., Rebeiz, M., Pardinas, J., Liu, L. and

Larson, J.H.

Bovine ESTs

Unpublished (2000)

Contact: Lewin, H. A.

W. M. Keck Center for Comparative and Functional Genomics

University of Illinois at Urbana-Champaign

340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL

61801, USA

Tel: 217 333 5998

Fax: 217 244 5617

Email: h-lewin@uiuc.edu

Funding for cattle EST sequencing was provided by the USDA National

Research Initiative, Animal Genome Resource Grant AG 99-3205-8534

to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED

from Washington University Genome Center. Vector Trimmi 9:

Cross match from Washington University Genome Center PHRAP suite.

This sequence is vector free and at least 200 bp in length. REPEAT

IN THE SEQUENCE Simple_repeat STRAND (+) ELEMENT (A)n LOCATION

[621,642].

PCR Primers

FORWARD: TAATACGACTCACTATAGGG

BACKWARD: ATTAACCTCTACTTAAG

Insert Length: 642 Std Error: 0.00

Plate: BP250008B10 row: E column: 9

Seq primer: AGCGATAACAATTTCACACAGGA

High quality sequence stop: 642.

Location/Qualifiers

1..642

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/mol_type="mRNA"

/db_xref="taxon:9913"

/clone="BP250008B10E9"

/sex="female"

/lab_host="DH10B"

/note="Organ: placenta; Vector: pT73Pac; Site 1: EcoRI;

Site 2: NotI; The cDNA library was contributed by the

Soares laboratory and it was constructed and normalized

as described by Bonaldo, M.F., Lennon, G. and Soares,

M.B. (1996), Genome Research 6(9): 791-806."

ORIGIN

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Best Local Similarity

Mismatches

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Indels

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profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

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Best Local Similarity 98.5%; Pred. No. 5.8e-62;
Matches 388; Conservative 0; Mismatches 2; Indels 4; Gaps 4;

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Db 406 GAGAGGATCAGCTCATCATCAACCCACACAGGCTGGAAGCCGAGCATCTCAGAGCCTA 347
    |||

QY 558 C-CTGGGAGTTGCTCATCTGCGGTCTATGCC-TGTGTCTCTCCCTGCCCTTCTCTGGCC 615
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Db 346 CACTGGGAGTTGCTCATCTGCGGTCTATGCCATGTCTCTCTCCCTGCCCTTCTCTGGCC 287
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QY 616 AACAGCATCTGGAGATGTCTTCCACAGACCA-CTCAAGGCTCTGAGTTCCTGGC 674
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Db 286 AACAGCATCTGGAGATGTCTTCCACAGACCACTCCAAAGGCTCTGGAGTTCCTGGC 227
    |||

QY 675 AGATAAGGTGTCTGTACCGAGTCTTGGCCACTGGCTCACACCGACCATCTACACCC 734
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Db 226 GATTAAGGTGTCTGTACCGAGTCTTGGCCACTGGCTCACACCGACCATCTACACCC 167
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QY 735 CTTCTGCTCTCTTCCAGTACTGCTCCCACTGGGCTTTCATCTGCTGTGTATGCAAG 794
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QY 795 CATCTACCGGCGCTGACAGGCGAGGCGCGGTTCACAGGCGACCTACAGCTTGG 854
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QY 855 AGCTGGGCACATGAAGCAGGTCAATGTGTGCTG 888
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LOCUS      Mus musculus NPY1R gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION      genomic survey sequence.
ACCESSION      AY413582
VERSION      AY413582.1 GI:39769544
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
      1 (bases 1 to 1149)
      Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
      Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
      Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
      Adams,M.D. and Cargill,M.
      Adams,M.D. and Cargill,M.
      Inferring nonneutral evolution from human-chimp-mouse orthologous
      gene trios
      Science 302 (5652), 1960-1963 (2003)
      14671302
      2 (bases 1 to 1149)
      Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
      Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
      Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
      Adams,M.D. and Cargill,M.
      Direct Submission
      Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
      Rockville, MD 20850, USA
      This sequence was made by sequencing genomic exons and ordering
      them based on alignment.
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      /mol_type="genomic DNA"
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RESULT 8
 BY733731
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

BY733731 679 bp mRNA linear EST 17-DEC-2002
 musculus CDNA clone G630073124 5', mRNA sequence.
 BY733731
 EST.
 BY733731.1 GI:27146858
 Mus musculus (house mouse)

Mus musculus
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 679)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
 Nikaide, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,
 Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
 Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C.,
 Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H.,
 Batalov, S., Beisel, K. W., Blake, J. A., Bratt, D., Brusic, V.,
 Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A.,
 Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T.,
 Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
 Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A.,
 Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A.,
 Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. B.,
 Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
 Numata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G.,
 Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S.,
 Ravasi, T., Reed, J. C., Reid, J., Reid, J., Ring, B. Z., Ringwald, M.,
 Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K.,
 Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M.,
 Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
 Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
 Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
 Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
 Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
 Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
 Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
 Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,
 Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 22354683
 12466851

Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P.,
 Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F.,
 Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,
 Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,
 Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N.,
 Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,
 Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission
 Computational Analysis of Full-length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site (http://genome.gsc.riken.go.jp) for
 further details.

FEATURES
 Location/Qualifiers
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 Best Local Similarity 74.5%; Pred. No. 3.5e-50;
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 Db 498 CCTACTCATTTGCCAACCCTGGCTTCTGTGACTTCCTCATGTGCTCTCATCTGCCACCAT 557
 QY 378 GACCGCGCTTACACCATCATGAGTCTGAGATCTTTGGAGAGACCCCTCTGCAAGATGTC 437
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 QY 438 GGCCTTCATCCAGTGCATGTGGTGAGGCTCCATCTCTCTGCTCTGCTCTGCTGGGCT 497
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 QY 498 GG 499
 Db 678 GG 679

RESULT 9
 AK030279 2570 bp mRNA linear HTC 18-SEP-2003
 LOCUS Mus musculus 11 days pregnant adult female ovary and uterus cDNA,
 DEFINITION RIKEN full-length enriched library, clone:5031404D23

product:NEUROPEPTIDE Y RECEPTOR TYPE 6, full insert sequence.
 AK030279
 VERSION AK030279.1 GI:26326262
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 20499374
 MEDLINE 11042159
 PUBLISHED 11042159
 3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
 Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 20530913
 MEDLINE 11076861
 PUBLISHED 11076861
 4 The RIKEN Genome Exploration Research Group Phase II Team and the
 FANTOM Consortium.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409, 685-690 (2001)
 5 The FANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 6 (bases 1 to 2570)
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
 Fukuda, S., Furuno, M., Hasegawa, T., Hara, A., Hashizume, M.,
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
 Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
 Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
 Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
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 Okazaki, Y., Saigo, R., Saichou, H., Sakai, C., Sakai, K., Sakazume, N.,
 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
 Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
 Fax: 81-45-503-9216)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site for further details.

URL: http://genome.gsc.riken.go.jp/
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 ORIGIN
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 Best Local Similarity 53.2%; Pred. No. 5, 1e-48;
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 QY 501 GAGGCATCAGCTCATCATCATCAACCAACAGGCTGGAAGCCAGCATCTCACAGGCTACCT 560

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES
source

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/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, adult male urinary bladder"
/note="Site 1: Sali; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGAGAGATCCAGAGCTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 370.0. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGATTCGAGTTAATAATTAATCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda Pfu I"

```

ORIGIN

Query Match	19.3%; Score 254.2; DB 10; Length 639;
Best Local Similarity	75.4%; Pred. No. 4e-43;
Matches 316; Conservative	0; Mismatches 103; Indels 0; Gaps 0;
QY	18 TGCTTGTAGGGCGTTCATCCCTCAAGTGTATCACTTAGTTCAAGAGTCCTGGAAATCTTTT 77
Db	221 TACCTGCCAGGTGCAATCTCTGAAGTAGCCCTTTTACTCTCTGGAGTTCCTGGATCTTCT 280
QY	78 CACATCCATATGAACACCTTCACCTTCCTCTGGCTTGTGCTCCCAAAATCTCCACAAGG 137
Db	281 CACACCTACCATGAATACCTCTCATTTCTTGGGCCCTCTCTTCCAGGATCCCTACAGGG 340
QY	138 TGAAPACAGAGCAAAACCCCTGGGCACCCCATACAACTCTCTGACATTTGCCAGGATTC 197
Db	341 TAAGAATGGACCAATCCATTTGAATTCGCCCTATAATTTCTCTGATGGCTSCCAGGATTC 400
QY	198 CGTGGACGTGATGGTCTTTCATCTCTCACTTCCTACAGCATTTGAGACTGTCGTGGGGTCCCT 257
Db	401 GGCAGAGCTGTGGCCCTTCATCATCACCACCTACAGCATTTGAGACCATCTTGGGGTCCCT 460
QY	258 GGGTAACCTCTGGCTGATGTGTGACTGTGAGGCGAGAGGAGAACGCCAAACGTGACCAA 317
Db	461 GGGAAACCTCTGCTTGATATTTGTGACCAACAAGAGAAAGTCCAATGTGACCAA 520
QY	318 CTTGCTTATCGCCAAACCTGGSCCTTCTCTGACTTCTCCTCATGTGCTCTCTGTGCCAGCGCT 377
Db	521 CCTGCTCATTGCACAACTGGCCCTCTCTGACTTCTCATGTGTGCTCATCTGCCAACCACT 580
QY	378 GACCGCGGTTACCAACCATCATGCACTACTGGATCTTTTGGAGAGACCCCTCTGCAAGATGT 436
Db	581 CACAGTCACCTACACCATCATGATTAATCTGCATCTTTGTGGAAGTCTTTTGCAGAATGT 639

RESULT 12					
AY413581					
LOCUS	AY413581	1152 bp	DNA	linear	GSS 17-DEC-2003
DEFINITION	Pan troglodytes NPY1R gene, VIRUAL TRANSCRIPT, partial sequence, genomic survey sequence.				
ACCESSION	AY413581				

864	GAATCATCAGATCATGTGCTACCTGTCGACACCAATCTGTTATTCCTGCTGCGCACTCAC	923
1017	TGCCATGGCCCTCCACCTGCGCTCAACCCATCATCTATGGCTTTCTCAACACCAACTTCAA	1076
924	AGCAATGATATCCACTTGTGTCGAACCCCATATTTTATGGTTCCTGAACAAAACATCCA	983
1077	GAAGGAGATCAAGGCCCTGCTGCTGACTTCCGACGACGAGCGCCCTCGAGAGATCGGA	1136
984	GAGAGACTTCGAGTTCCTCTTCAACTTTTGTGATTTCCGGTCTCGGAGATGATTATGA	1043
1137	GCATCTGCCCTGTCCACAGTACATACGGAAGTCTCCAAAAGGTCCCTGAGGCTAAAGTG	1196
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1197	CAGGTCCAATCCCAATTTAAACAGGTCTA	1224
1100	CAAGCCCAAGTCGCAATTTAAAAAATCAA	1127

RESULT 11	BB628025	639 bp	mrna	linear	EST 26-OCT-2001
BB628025	BB628025	RIKEN full-length enriched,	adult male urinary bladder Mus		
LOCUS	BB628025	musculus cDNA clone 9530057L11 5',	mrna sequence.		
DEFINITION	BB628025	BB628025.1	GI:16465558		
ACCESSION	BB628025	Mus musculus (house mouse)			
VERSION	BB628025.1	Mus musculus			
KEYWORDS	EST,				
SOURCE	Mus musculus				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
	1 (bases 1 to 639)				
	Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,				
	Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,				
	Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,				
	Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,				
	Sano,H., Saeki,D., Shibata,K., Shinagawa,A., Shiraki,T.,				
	Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,				
	Takeda,Y., Tanaka,T., Toyota,T., Muramatsu,M. and Hayashizaki,Y.				
	RIKEN Mouse ESTs (Arakawa,T., et al. 2001)				
TITLE	Unpublished (2001)				
JOURNAL					
COMMENT	Contact: Yoshihide Hayashizaki				
	Laboratory for Genome Exploration Research Group, RIKEN Genomic				
	Sciences Center (GSC), Yokohama Institute				
	The Institute of Physical and Chemical Research (RIKEN)				
	1-7-22 Suehiro-cho, Teurumi-Ku, Yokohama, Kanagawa 230-0045, Japan				
	Tel: 81-45-503-9222				
	Fax: 81-45-503-9216				

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VERSION      AY413581.1  GI:39769543
KEYWORDS     GSS.
SOURCE       Pan troglodytes (chimpanzee)
ORGANISM     Pan troglodytes
REFERENCE    1 (bases 1 to 1152)
AUTHORS      Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
              Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
              Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
              Adams,M.D. and Cargill,M.
TITLE        Inferring nonneutral evolution from human-chimp-mouse orthologous
              gene trios
JOURNAL      Science 302 (5652), 1960-1963 (2003)
PUBMED       14671302
REFERENCE    2 (bases 1 to 1152)
AUTHORS      Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
              Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
              Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
              Adams,M.D. and Cargill,M.
TITLE        Direct Submission
JOURNAL      Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
              Rockville, MD 20850, USA
COMMENT      This sequence was made by sequencing genomic exons and ordering
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DB 90 TGAATGATTGTCATCTGCCCTTGGCCATGATATTTACCTTAGCTCTTGTCTATGGAGCTGT 149
QY 240 GACTGTCTGGGGGCTCCTGGGTAACCTCTGCCTGATGTGTGACTGTGTGAGCGACGAAGA 299
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DB 150 GATCATCTCTGTGGTGTCTCTGGAAACCTGGCCTTGATCATATCATCTTGAACAAAGA 209
QY 300 GAAAGCCACGTGACCAACCTGTTATCGCAACCTGGCCTTCTCTGACTTCTCTCATGTG 359
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DB 210 GATGAGAAATGTTACCAACATCCTGATTTGTGAACCTTTCTTCAGACTTCTGTTTGC 269
QY 360 CTTCTCTGCGACCGCTGACCGCTCTACACCATCATGGAATCTTGGATCTTTGGAGA 419
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DB 270 CATCATGTCTCCCTTTACATTTCTTACACATTAATGGACCCTGGCTTTTGGTGA 329
QY 420 GACCTCTCTGCAAGATGTGGCCCTTTCATCCAGTGCATGTGCGTACGGTCTCCATCTCTC 479
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DB 330 GGGGATGTGTAGTTGAATCCCTTTTGTGCAATGTGTTTCAATCACTGTGTCCATTTCTC 389
QY 480 GCTCGTCTCTGGCCCTCGAGAGGATCAGCTCATCATCAACCAACAGGCTGGAGGC 539
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DB 390 TCTGGTCTCATCTGCTGTGGAACGACATCAGCTGATTAATCAACCTTCGAGGTGGAGCC 449
QY 540 CAGCATCTCAGAGCCTACCTGGGATTTGCTCAFTCTGGGTCAITGCTGTGCTCTCTC 599
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QY 600 CTTGCCCTCTCTGGCCCAAGCATCTGGAGATGCTTCCACAGAACCATCTCCAGGC 659
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DB 510 TTTGCTCTTCTGATCTACCAAGTATGACTGATG-----AGCCATTCCAAATGTATAC 563
QY 660 TCTGGAGTTCCTGGCAGATAAGGTGCTGTGTACCGAGTCTCGCCACTGGCTCACCACCG 719
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DB 564 ACTTGATGCATACAAAGACAAATACATGCTGCTTTGATCAATTTCCATCGACTCTCATAG 623
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QY 780 GGTCTGTATTGACGCAATCTACCGGGCCCTGACAGAGCGAGGGCGGTGTTTCCACAA--- 836
DB 684 TATTGCTACTTCAAGATATATATACGCTTAAAGAGGAGAAACAACATGATGACAAGAT 743
QY 837 GGCACCTACAGCTTGGAGCTGGGACATGAAGCAGGTCAATGTGGTCTGCTGGTGTGAT 896
DB 744 GAGAGACAATAGTACAGGTCCAGTGAACCAAGAAATCAATATCATGCTGCTCTCCAT 803
QY 897 GGTGGTGGCCCTTTGGCGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 956
DB 804 TGTGGTAGCGTTTGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 863
QY 957 GCACCATGAGGCCATCCCATCTGCTGCGACGGAACCTCATCTTCTTAGTGTGCCACTGTCT 1016
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QY 1077 GAAGGAGATCAAGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1136
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QY 1197 CAGTCCCAATCCCAATTTAACAGGTCTA 1224
DB 1100 CAAGCCAGTGCATTTTAAAAAATCAA 1127

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DEFINITION AGENCOURT 8967758 NIH_MGC_94 Mus musculus cdna clone IMAGE:6490858
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ACCESSION BUB40743
VERSION   BUB40743.1  GI:24025143
KEYWORDS  EST.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
REFERENCE 1 (bases 1 to 936)
AUTHORS   NIH-MGC http://mgs.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgabs-t@mail.nih.gov
          Tissue Procurement: The Cepko Laboratory
          cdna Library Preparation: Life Technologies, Inc.
          DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
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Site 2: SalI; Cloned unidirectionally; oligo-dr primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN	Query Match	14.1%;	Score 185.8;	DB 13;	Length 936;
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QY	180	TGAACATGCGAGATTCCTGACGATGCTCTTCATCGTCACCTCTCTACAGCATTTGA	239		
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QY	240	GACTGTCTGGGGTCTCTGGTAACTCTCCCTGATGTGTGCTGACGTGTGAGGCGAGAAGGA	299		
DB	284	GATTAATCTTGGGTCTCTGGAACCTGGCATTTGATCATTAATCATTTCTGAACAGAGAAGGA	343		
QY	300	GAAGCCAAAGTGACCACTGCTTATTCGCCAACCTGGCTCTCTGACTTCTCATGTG	359		
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QY	360	CCTCTCTGCGAGCGCTGACCGCGCTACACCATCATGACTTACTGGATCTTTGGAGA	419		
DB	404	GGTCATGTGCTCCCGTCTACTTTGTATATACATGATGACCACTGGGTCTTCGGGA	463		
QY	420	GACCTCTGCAAGATGCGGCTTCATCCAGTGCAATGCGTGACGGTCTCCATCTCTCTC	479		
DB	464	GACCATGTCAAACTGAATCCCTTTGTACAGTGTGTCTCCATCACAGTATCCATTTCTC	523		
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DB	584	AAACAATAGACATGCTTACATAGGATTAATGCTCAATTTGGGTCTTGCAGTGGCTCTCTC	643		
QY	600	CCTGCCCTCTGCGCAACAGCATCTCTGGAGATGTCTTCCACAGAACCACTCCAGGC	659		
DB	644	CTGCTCTTGTGATCTATCAATCTTGACCGAGAGCCCTTTCAAAATGTGCACTTGC	703		
QY	660	CTGGAGTCTCTGCGAGATAGGTGCTGTACCGAGTCTCTGCGCACTGGCTCACCACCG	719		
DB	704	---GGCGTTCAAGGACAGTATGTGTGTTGACAAATC---CCATCTGACTCTCACAG	756		
QY	720	CACATCTACACACCTCTCTCTCTCTCTCCAGTACTGCTCCCACTGGCTTCACTCT	779		
DB	757	GCTGTCTTACAGACT	816		
QY	780	GGTCTGTATTGACCGCATCTACCGCGCTCTGACAGGCGAGGCGGCGTGTTCACAGGG	839		
DB	817	CATATGCTACTTCAAGATATACATTCCTCCCTTGAAAGAGAGAACAACATTGATGACAAGAT	876		
QY	840	CAC 842			
DB	877	CCC 879			

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BX506438
ACCESSION
BX506438
VERSION
BX506438.1 GI:32046673
KEYWORDS
EST.
SOURCE
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ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 669)
Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R.,
Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
Wiemann,S.
EST (Poustka,A., Albert,R., Moosmayer,P., Schupp,I.,
Wellenreuther,R., et al.)
Unpublished (2003)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
Sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No si sequence available.
This clone (DKFzp779B1117) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
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QY	347	ACTTCTCTCATGTGCTCTCTGCGAGCGCTGACCGGCTGACACCATCATGACTACT	406		
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QY	407	GGATCTTTGGAGAGACCTCTGCAAGATGTGCGCTTTCATCCAGTGCATGCGGTGAGG	466		
DB	131	GGGTCTTTGGTGGCGGATGTGTAAGTTGAATCCTTTGTGCAATGTGTTCAATCACTG	190		
QY	467	TCTCCATCTCTCTGCTGCTCTGCGGCTTGGAGAGCATCAGCTCATCATCAACCCAA	526		
DB	191	TGTCCATTTCTCTGCTTCTCATTTGCTGTTGGAACGACATCAGCTGATATCAACCTC	250		
QY	527	CAGGCTGGAAGCCCAAGCATCTCACAGGCTACCTGGGATTTGCTCATCTGGGTCAATTG	586		
DB	251	GAGGTGGAGACCAATAATAGACATGCTTATGAGGTATTGCTGTGATTGGGTCTTTG	310		
QY	587	CTGTGTCTCTCTCTGCTCTCTGCGCAACAGCATCTGAGAAATGTCTTCCACAAGA	646		
DB	311	CTGTGGCTCTCTCTTGTGCTTCTCTGATCTACCAAGTAATGACTGATG-----AGCGT	364		
QY	647	ACCACTCCAAAGGCTCTGGAGTTCTTGGCAGATAAGTGTCTGTACCGAGTCTCTGGCCAC	706		
DB	365	TCCAAATGTAACTTGTGATGCTACAAAGACAATAGTGTGCTTGTATCAATTTCCAT	424		
QY	707	TGGCTCACACGCGACCATCTACACCACTTCTGCTCTCTCTTCCAGTACTGCTCCAC	766		
DB	425	CGGACTCTCATAGGTGTCTTATACCACTCTCTCTCTGCTGCTGAGTATTTTGGTCCAC	484		
QY	767	TGGGCTCTCATCTGCTGCTTATGCAAGCATCTACCGGCTGCTGAGAGGAGGCGGCG	826		
DB	485	TTTGTTTATTTATTTTGTCTTCTTCAAGATATATATACGCTTAAAGAGGAGAACACA	544		

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443	TC	ATTC	AGTGC	ATGTCG	TGACG	GTCTCA	TCTCTCT	CGCTCGTCTCGTGTGGCCCTCGAGA	502
416	TC	CTG	CAGCGGT	CACCGT	CTATG	TGTGG	GTTCAC	GGCTCACCA	475
503	GG	CA	TACG	CTCAT	CAAC	CCAA	CAGG	CTGGA	562
476	GC	TAC	GTG	GTCTGG	TGC	ACCCG	CTGAG	CGGCG	535
563	GG	AT	TGTG	CTATCT	CGGT	CAATG	CGCTCT	CCCTGCTTCTTGGCCAA	622
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656	AG	CG	CCAG	CGCC	AGCT	CTAC	CGC	CTGGG	715
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818	GC	CG	CG	CA	CTT	CTG	CTG	CTG	874
923	TG	CT	CT	GC	AT	GT	TTCAA	CAG	982
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983	AC	GG	GA	AC	CT	CA	TTCT	TAG	1042
935	CT	TT	GG	CG	CT	GT	CT	GC	994
1043	CA	TT	CA	CT	AT	TGG	CTT	CT	1102
995	CT	TC	AT	CT	AC	CG	CT	TC	1054
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1055	CT	TC	GC	1060					

ORIGIN

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QY	266	TCTGCCTGATGTGTGATCTGTGAGGCAGAGGAGAAAGCCACGTGACCAACCTGCCTTA	325		
Db	236	GCCTCGTGGTGTGTTATCGCGGGGTGGCCGGCTGCACACGTGACGAACTCTCTCA	295		
QY	326	TGGCAAACCTGGCCTTCTGACTTCCTCATATGTGCTCTCTCCCAAGCCGTGACCGCGG	385		
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QY	386	TCTACACCATCATG---GACTACTGGATCTTTGGAGAGACCTCTCTGCAAGATGTGGGCT	442		

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 11, 2004, 10:03:02 ; Search time 116 Seconds
(without alignments)
6314.958 Million cell updates/sec

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Perfect score: 1320
Sequence: 1 AGATTGTTTCTGTTTGC.....CCAGCATTCCTGGTTTCTG 1320

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
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5: /cgn2_6/ptodata/2/ina/PCUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1320	100.0	1320	1	US-08-176-412-1
2	1320	100.0	1320	2	US-08-555-268A-1
3	1320	100.0	1320	2	US-08-495-695B-1
4	1320	100.0	1320	5	PCT-US94-14436-1
5	1180	89.4	1180	4	US-09-016-434-1061
6	810.8	61.4	1439	5	PCT-US94-14436-27
7	810.8	61.4	1439	2	US-08-495-695B-27
8	278.6	21.1	2280	1	US-08-415-818-5
9	278.6	21.1	2280	5	US-08-894-236-5
10	278.6	21.1	2280	5	PCT-US96-01444-5
11	266	20.2	1439	1	US-08-415-818-11
12	266	20.2	1439	2	US-08-894-236-11
13	266	20.2	1439	5	PCT-US96-01444-11
14	257.6	19.5	1152	3	US-09-045-186-1
15	257.6	19.5	1152	3	US-09-045-186-3
16	257.6	19.5	1605	4	US-09-676-970-1
17	257.6	19.5	1605	4	US-09-676-972B-1
18	257.6	19.5	1605	4	US-09-016-434-1231
19	257.6	19.5	1605	4	US-08-876-941A-1
20	257.6	19.5	1605	4	US-10-013-846-3
21	257.6	19.5	2624	1	US-08-232-144-3
22	255.6	19.4	1957	4	US-09-016-434-1169
23	244.8	18.5	1338	5	PCT-US93-05039-1
24	244.8	18.5	1534	5	PCT-US93-05039-2
25	173.6	13.2	595	1	US-08-784-289-1
26	159.8	12.1	4571	1	US-08-232-144-5
27	156	11.8	1110	3	US-08-513-974B-31

28 156 11.8 1110 3 US-08-776-971-26 Sequence 26, Appl
29 156 11.8 1110 4 US-09-461-436B-31 Sequence 31, Appl
30 156 11.8 1110 4 US-09-170-496D-177 Sequence 177, Appl
31 156 11.8 1331 3 US-08-513-974B-322 Sequence 322, Appl
32 156 11.8 1331 3 US-08-776-971-103 Sequence 103, Appl
33 152.8 11.6 1110 4 US-09-170-496D-25 Sequence 25, Appl
34 152.8 11.6 1535 4 US-09-016-434-1051 Sequence 1051, Appl
35 147.2 11.2 1113 3 US-09-172-353-1 Sequence 1, Appl
36 147.2 11.2 1113 3 US-09-799-955-1 Sequence 1, Appl
37 138.2 10.5 1293 3 US-09-255-368-7 Sequence 7, Appl
38 137.6 10.4 1116 3 US-08-776-971-139 Sequence 139, Appl
39 128.2 9.7 1200 4 US-09-016-434-1062 Sequence 1062, Appl
40 128.2 9.7 1280 1 US-08-192-288-1 Sequence 1, Appl
41 128.2 9.7 1280 2 US-08-687-355A-1 Sequence 1, Appl
42 128.2 9.7 1280 4 US-09-407-367-1 Sequence 1, Appl
43 126 9.5 1200 2 US-08-687-355A-5 Sequence 5, Appl
44 126 9.5 1200 4 US-09-407-367-5 Sequence 5, Appl
45 125 9.5 2144 4 US-08-876-798A-1 Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-176-412-1
; Sequence 1, Application US/08176412
; Patent No. 5516553
; GENERAL INFORMATION:
; APPLICANT: Bard, Jonathan A.
; APPLICANT: Walker, Mary
; APPLICANT: Branchek, Theresa
; APPLICANT: Weinshank, Richard L.
; TITLE OF INVENTION: DNA ENCODING A HUMAN NEUROPEPTIDE
; TITLE OF INVENTION: Y/PEPTIDE YY/PANCREATIC POLYPEPTIDE
; TITLE OF INVENTION: RECEPTOR (Y4) AND USES THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/176.412
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/POCKET NUMBER: 44743/JPW/TEP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1320 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 88..1212
; US-08-176-412-1

Query Match		100.0%;	Score 1320;	DB 1;	Length 1320;	
Best Local Similarity		100.0%;	Pred. No. 0;			
Matches 1320;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	1	AGTATTCTTTGTCGTTTGGCTTGTAGGGGCTCATCCCTCAAGTGATCACTTAGTTCAA	60			
Db	1	AGTATTCTTTGTCGTTTGGCTTGTAGGGGCTCATCCCTCAAGTGATCACTTAGTTCAA	60			
Qy	61	GAGTCCTGGGAATCTTTTACATCCACTATGAACACCTCTCACCTCCCTGGCCCTTGCTGCTC	120			
Db	61	GAGTCCTGGGAATCTTTTACATCCACTATGAACACCTCTCACCTCCCTGGCCCTTGCTGCTC	120			
Qy	121	CCAAATCTCCAGAGTGAACAGAGCAAGCAACCCCTGGGACCCCATACACTTCTCT	180			
Db	121	CCAAATCTCCAGAGTGAACAGAGCAAGCAACCCCTGGGACCCCATACACTTCTCT	180			
Qy	181	GAACATTGCCAGGATTCGGTGAGCGTGATGCTCTTCACTCGCTCACTTCTTACAGCATTTGAG	240			
Db	181	GAACATTGCCAGGATTCGGTGAGCGTGATGCTCTTCACTCGCTCACTTCTTACAGCATTTGAG	240			
Qy	241	ACTGTCTGGGGTCTCTGGGTAACTCTGCTGATGTGTGACTGTGAGCGCAGAGGAG	300			
Db	241	ACTGTCTGGGGTCTCTGGGTAACTCTGCTGATGTGTGACTGTGAGCGCAGAGGAG	300			
Qy	301	AAAGCCAACTGACCAACCTCTTATCGCAACCTGACCTTCTCTGACTTCTCTCATGTGC	360			
Db	301	AAAGCCAACTGACCAACCTCTTATCGCAACCTGACCTTCTCTGACTTCTCTCATGTGC	360			
Qy	361	CTCTCTGCCAGCGCTGACCGCGTCTACCAATCATGACTGTGATCTTGTGAGAG	420			
Db	361	CTCTCTGCCAGCGCTGACCGCGTCTACCAATCATGACTGTGATCTTGTGAGAG	420			
Qy	421	ACCTCTGCAAGATGTGGCCTTCTCATCGAGCATGTCGGTGAGGCTCTCCATCTCTCG	480			
Db	421	ACCTCTGCAAGATGTGGCCTTCTCATCGAGCATGTCGGTGAGGCTCTCCATCTCTCG	480			
Qy	481	CTCGTCTCTGCGCCCTGGAGAGCATCAGCTCATCATCAACCAACAGGCTGGAAGCCC	540			
Db	481	CTCGTCTCTGCGCCCTGGAGAGCATCAGCTCATCATCAACCAACAGGCTGGAAGCCC	540			
Qy	541	AGCATCTACAGGCTACCTGGGATTTGCTCATCTGGGTCTATGCTGCTGCTCTCTCC	600			
Db	541	AGCATCTACAGGCTACCTGGGATTTGCTCATCTGGGTCTATGCTGCTGCTCTCTCC	600			
Qy	601	CTGGCTTCTTCTGGCAACAGCATCTCTGGAGATCTTTCACAGAACCACTCCAAAGGCT	660			
Db	601	CTGGCTTCTTCTGGCAACAGCATCTCTGGAGATCTTTCACAGAACCACTCCAAAGGCT	660			
Qy	661	CTGAGATCTCTGGCAGATAGGTGGTCTGTACCGAGTCTGCGCACTGCGTCAACCCGC	720			
Db	661	CTGAGATCTCTGGCAGATAGGTGGTCTGTACCGAGTCTGCGCACTGCGTCAACCCGC	720			
Qy	721	ACCATCTACACACCTTCTCTCTCTTCCAGTACTGCTTCCACCTGGGCTTCTCATCTG	780			
Db	721	ACCATCTACACACCTTCTCTCTCTTCCAGTACTGCTTCCACCTGGGCTTCTCATCTG	780			
Qy	781	GTCTGTTATGACGATCTACCGGCGCTGACAGAGGAGGGCGCGCTGTTTCAAGGGC	840			
Db	781	GTCTGTTATGACGATCTACCGGCGCTGACAGAGGAGGGCGCGCTGTTTCAAGGGC	840			
Qy	841	ACCTACAGCTTGGAGCTGGGCAATGAAGCAGGTCAATGTGTGCTGCTGGTGTATGGT	900			
Db	841	ACCTACAGCTTGGAGCTGGGCAATGAAGCAGGTCAATGTGTGCTGCTGGTGTATGGT	900			
Qy	901	GTGGCTTTGGCGTCTGTGGCTGTCTGATGTGTTTCAACAGCTGGAGAGTGGCAC	960			
Db	901	GTGGCTTTGGCGTCTGTGGCTGTCTGATGTGTTTCAACAGCTGGAGAGTGGCAC	960			
Qy	961	CATGAGGCATCCCATCTGCAAGGAACTCTCTTCTTGTGTGCTCACTTCTCTGCC	1020			
Db	961	CATGAGGCATCCCATCTGCAAGGAACTCTCTTCTTGTGTGCTCACTTCTCTGCC	1020			

Query Match
Best Local Similarity

100.0%; Score 1320; DB 2; Length 1320;
100.0%; Pred. No. 0;

RESULT 2

US-08-555-268A-1

; Sequence 1, Application US/08555268A

; Patent No. 5958709

; GENERAL INFORMATION:

; APPLICANT: Bard, Jonathan A.

; APPLICANT: Walker, Mary

; APPLICANT: Branchek, Theresa

; APPLICANT: Weinshtank, Richard L.

; TITLE OF INVENTION: DNA ENCODING A HUMAN NEUROPEPTIDE

; TITLE OF INVENTION: Y/PEPTIDE YV/PANCREATIC POLYPEPTIDE

; TITLE OF INVENTION: RECEPTOR (Y4) AND USES THEREOF

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper & Dunham LLP

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/555,268A

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 44743-Z/JPW/MAT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 278-0400

; TELEFAX: (212) 391-0526

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1320 base pairs

; TYPE: nucleic acid

; TOPOLOGY: linear

; STRANDEDNESS: single

; MOLECULE TYPE: DNA (genomic)

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 88..1212

; US-08-555-268A-1

Matches 1320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTATTGTTGCTGTTGCTTGTAGGGCGTATCCCTCAAGTGTATCACTAGTTCAA 60

Db 1 AGTATTGTTGCTGTTGCTTGTAGGGCGTATCCCTCAAGTGTATCACTAGTTCAA 60

QY 61 GASTCCTGGATCTTTTACATCAGTATGACCTCTACCTCTACCTCCCTGGCTTGTCTCTC 120

Db 61 GASTCCTGGATCTTTTACATCAGTATGACCTCTACCTCTACCTCCCTGGCTTGTCTCTC 120

QY 121 CCAAAATCTCCACAGTGTAAAGACAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 180

Db 121 CCAAAATCTCCACAGTGTAAAGACAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 180

QY 181 GAACTTCCAGAGATTCCTGCGAGTGTATGCTTCTATCTCTATCTCTATCTCTATCTCT 240

Db 181 GAACTTCCAGAGATTCCTGCGAGTGTATGCTTCTATCTCTATCTCTATCTCTATCTCT 240

QY 241 ACTGTCTGGGGGCTCTCTGGGTAACTCTCTGCTGATGTGTGTGACTGTGAGGCAAGAG 300

Db 241 ACTGTCTGGGGGCTCTCTGGGTAACTCTCTGCTGATGTGTGTGACTGTGAGGCAAGAG 300

QY 301 AAAGCCAAAGTACCAAGCTGTTATGCGCAACCTGGGCTTCTCTGACTTCTCTATGTC 360

Db 301 AAAGCCAAAGTACCAAGCTGTTATGCGCAACCTGGGCTTCTCTGACTTCTCTATGTC 360

QY 361 CTCCTCTGCGAGCGCTGACGCGCTTACACCATCATGGACTACTGATCTTTGGAGAG 420

Db 361 CTCCTCTGCGAGCGCTGACGCGCTTACACCATCATGGACTACTGATCTTTGGAGAG 420

QY 421 ACCCTCTGAGAGTGTGGCTTCTTACAGTGTATGCTGCTGAGCGTCTCCATCTCTCTG 480

Db 421 ACCCTCTGAGAGTGTGGCTTCTTACAGTGTATGCTGCTGAGCGTCTCCATCTCTCTG 480

QY 481 CTCGCTCTGCGGCTCTGGAGAGGATCAGCTCATCAACCAAGGCTGGAAGGCC 540

Db 481 CTCGCTCTGCGGCTCTGGAGAGGATCAGCTCATCAACCAAGGCTGGAAGGCC 540

QY 541 AGCATCTCACAGGCTTACCTGGGGATGTGTCTCATCTGGGTCAATGCTGTCTCTCTCC 600

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Db 601 CTGCGCTTCTGGCCAAAGCATCTGGAGATGCTTCCCAAGCAAGCAAGCAAGCAAGCT 660

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QY 721 ACCATCTACACCTTCT 780

Db 721 ACCATCTACACCTTCT 780

QY 781 GTCTGTATGACGATCTACCGGCGCTGACAGAGCGAGGCGGCTGTTTCAAGAGGC 840

Db 781 GTCTGTATGACGATCTACCGGCGCTGACAGAGCGAGGCGGCTGTTTCAAGAGGC 840

QY 841 ACTACAGCTTGGAGCTGGGCACTGAAGAGAGTCAATGTGTGTGTGTGTGTGTGTGTGT 900

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QY 901 GTGGCTTGTGCGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960

Db 901 GTGGCTTGTGCGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960

QY 961 CATGAGGCAATCCCACTGCGCAAGGCAAGCTCATCTCTTGTGTGTGTGTGTGTGTGTGT 1020

Db 961 CATGAGGCAATCCCACTGCGCAAGGCAAGCTCATCTCTTGTGTGTGTGTGTGTGTGTGT 1020

QY 1021 ATGGCTTCCAGCTGCTGCAAGCAATCTATGCTGCTTCTCAACCAAGCAAGCAAGCAAG 1080

Db 1021 ATGGCTTCCAGCTGCTGCAAGCAATCTATGCTGCTTCTCAACCAAGCAAGCAAGCAAG 1080

RESULT 3

US-08-495-695B-1
; Sequence 1, Application US/08495695B
; Patent No. 5976814
; GENERAL INFORMATION:
; APPLICANT: Baird, Jonathan A.
; APPLICANT: Walker, Mary
; APPLICANT: Branchek, Theresa
; APPLICANT: Weinshank, Richard L.
; TITLE OF INVENTION: DNA ENCODING A HUMAN NEUROPEPTIDE
; TITLE OF INVENTION: Y/PEPTIDE YV/PANCREATIC POLYPEPTIDE
; TITLE OF INVENTION: RECEPTOR (Y4) AND USES THEREOF
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036

COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/495,695B
; FILING DATE: 13-Jan-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44743-A-PCT-US/JPW/JHB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1320 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 88..1212
; US-08-495-695B-1

Query Match 100.0%; Score 1320; DB 2; Length 1320;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTATTGTTGCTGTTGCTTGTAGGGCGTATCCCTCAAGTGTATCACTAGTTCAA 60

Db 1 AGTATTGTTGCTGTTGGCTTGTAGGGCGTCATCCCTCAAGTGTATCACCTTAGTTCAA 60
Qy 61 GAGTCTGGATCTTTTACATCCATATGACACCTCTCACTCTCTGCTGCTGCTGCTC 120
Db 61 GAGTCTGGATCTTTTACATCCATATGACACCTCTCACTCTCTGCTGCTGCTGCTC 120
Qy 121 CCAAAATCTCCAAGAGTGAAGGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 180
Db 121 CCAAAATCTCCAAGAGTGAAGGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 180
Qy 181 GAACATGCGAGATTCCTGGAGCGTATGCTTCTATGCTGCTATCTCTTCTACAGCAATGAG 240
Db 181 GAACATGCGAGATTCCTGGAGCGTATGCTTCTATGCTGCTATCTCTTCTACAGCAATGAG 240
Qy 241 ACTGTCTGGGGGTCTCTGGGTAACTCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Db 241 ACTGTCTGGGGGTCTCTGGGTAACTCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Qy 301 AAGCCAACTGACCACTGCTTATGCGCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Db 301 AAGCCAACTGACCACTGCTTATGCGCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Qy 361 CTCTCTGCGAGCGCTGACCGCGTCTACCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Db 361 CTCTCTGCGAGCGCTGACCGCGTCTACCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Qy 421 ACCCTCTGCAAGATGTCGGCTTCTATCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db 421 ACCCTCTGCAAGATGTCGGCTTCTATCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Qy 481 CTGCTCTCTGCGCTGCGAGGATCAGCTCATCATCAACCAAGCTGCTGCTGCTGCTGCTGCTG 540
Db 481 CTGCTCTCTGCGCTGCGAGGATCAGCTCATCATCAACCAAGCTGCTGCTGCTGCTGCTGCTG 540
Qy 541 AGCATCTCAGAGGCTACCTGGGATGCTCATCTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Db 541 AGCATCTCAGAGGCTACCTGGGATGCTCATCTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Qy 601 CTGCGCTCTGCGCAAGCATCTGGAGATGCTTCCACAGCAAGCAAGCAAGCAAGCAAGCAAG 660
Db 601 CTGCGCTCTGCGCAAGCATCTGGAGATGCTTCCACAGCAAGCAAGCAAGCAAGCAAGCAAG 660
Qy 661 CTGAGATCTCTGGCAGATGAGTGTCTGTACCGAGTCTTGGCAGTCTGCTGCTGCTGCTGCTG 720
Db 661 CTGAGATCTCTGGCAGATGAGTGTCTGTACCGAGTCTTGGCAGTCTGCTGCTGCTGCTGCTG 720
Qy 721 ACCATCTACACATCTCTGCTCTCTCTTCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db 721 ACCATCTACACATCTCTGCTCTCTCTTCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Qy 781 GTCTGTTATGACGATCTACCGCGCTGCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 840
Db 781 GTCTGTTATGACGATCTACCGCGCTGCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 840
Qy 841 ACCTACAGCTTGGAGCTGGGCAATGAGCAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Db 841 ACCTACAGCTTGGAGCTGGGCAATGAGCAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Qy 901 GTGGCTTTGGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Db 901 GTGGCTTTGGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Qy 961 CATGAGGCACTCCCATCTGCGACGGGAACTCATCTTCTTCTGCTGCTGCTGCTGCTGCTGCTG 1020
Db 961 CATGAGGCACTCCCATCTGCGACGGGAACTCATCTTCTTCTGCTGCTGCTGCTGCTGCTGCTG 1020
Qy 1021 ATGGCTCCACCTGGTCAACCCATTCATCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
Db 1021 ATGGCTCCACCTGGTCAACCCATTCATCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
Qy 1081 GAGATCAAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140

Db 1081 GAGATCAAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
Qy 1141 CTGCCCCCTGTCACAGTACATACGGAAGTCTCCAAAGGGTCTCCCTGAGGCTAAGTGGCAGG 1200
Db 1141 CTGCCCCCTGTCACAGTACATACGGAAGTCTCCAAAGGGTCTCCCTGAGGCTAAGTGGCAGG 1200
Qy 1201 TCCAATCCCATTTAAACAGGCTAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
Db 1201 TCCAATCCCATTTAAACAGGCTAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
Qy 1261 CACTTAGTCTAAGTGGGACACTGCAAGCTGGGTGGCAGCCAGCATTCCTGGCTTTCTG 1320
Db 1261 CACTTAGTCTAAGTGGGACACTGCAAGCTGGGTGGCAGCCAGCATTCCTGGCTTTCTG 1320

RESULT 4
PCT-US94-14436-1
; Sequence 1, Application PC/TUS9414436
; GENERAL INFORMATION:
; APPLICANT: Bard, Jonathan A.
; APPLICANT: Walker, Mary
; APPLICANT: Branchek, Theresa
; APPLICANT: Weinschank, Richard L.
; TITLE OF INVENTION: DNA ENCODING A HUMAN NEUROPEPTIDE
; TITLE OF INVENTION: Y/PEPTIDE YV/PANCREATIC POLYPEPTIDE
; TITLE OF INVENTION: RECEPTOR (Y4) AND USES THEREOF
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/14436
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44743-A-PCT\JPW\WAT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1320 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 88..1212
; PCT-US94-14436-1

Query Match 100.0%; Score 1320; DB 5; Length 1320;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGTATTGTTGCTGTTTGGCTTGTAGGCGGTCATCCCTCAAGTGTATCACCTTAGTTCAA 60
Db 1 AGTATTGTTGCTGTTTGGCTTGTAGGCGGTCATCCCTCAAGTGTATCACCTTAGTTCAA 60
Qy 61 GAGTCTGGATCTTTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCT 120

121 GAACATTGCCAGGATTCGGTGGAGCTGATGGTCTTCATCGTCACCTTCCTACAGCATTGAG 180
241 ACTGTGTGGGGTCTCGGTAACTCTGCTGATGTGTGCTGACTGTGAGCGAGAGGAG 300
181 ACTGTGTGGGGTCTCGGTAACTCTGCTGATGTGTGCTGACTGTGAGCGAGAGGAG 240
301 AAAGCCAACTGACCAACTCTTATCGCCAACTCGGCTTCTCTGACTTCTCTCATGTGC 360
241 AAAGCCAACTGACCAACTCTTATCGCCAACTCGGCTTCTCTGACTTCTCTCATGTGC 300
361 CTCCTCTGCCAGCGCTGACCGCGTCTACACATCATGAGCACTACTGATCTTTGAGAG 420
301 CTCCTCTGCCAGCGCTGACCGCGTCTACACATCATGAGCACTACTGATCTTTGAGAG 360
421 ACCCTCTGCAAGATGTGGCGCTTCATCCAGTGCATGTGCGGTGACGGTCTCCATCTCTCG 480
361 ACCCTCTGCAAGATGTGGCGCTTCATCCAGTGCATGTGCGGTGACGGTCTCCATCTCTCG 420
481 CTCCTCTGTGGCGCTGGAGAGCATCAGTCTATCATCAACCAACAGCGCTGGAGCGCC 540
421 CTCCTCTGTGGCGCTGGAGAGCATCAGTCTATCATCAACCAACAGCGCTGGAGCGCC 480
541 AGCATCTACAGGCTACCTCGGATGTGCTCATCTGGGTCTATTGCTGTGCTCTCTCC 600
481 AGCATCTACAGGCTACCTCGGATGTGCTCATCTGGGTCTATTGCTGTGCTCTCTCC 540
601 CTGCGCTTCTGGCCAAACAGCATCTCGAGATGCTTCCAAAGAACCACTCCAAAGGCT 660
541 CTGCGCTTCTGGCCAAACAGCATCTCGAGATGCTTCCAAAGAACCACTCCAAAGGCT 600
661 CTGAGATCTCGGAGATAGTGGTCTGTACCGAGTCTGGGCTGCTGCTGCTGCTGCTGCTG 720
601 CTGAGATCTCGGAGATAGTGGTCTGTACCGAGTCTGGGCTGCTGCTGCTGCTGCTGCTG 660
721 ACCATCTACACACCTTCT 780
661 ACCATCTACACACCTTCT 720
781 GTCTGTTATGACGCTACCGGCTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
721 GTCTGTTATGACGCTACCGGCTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
841 ACCTACAGCTTGCAGCTGGGACATGAAGCAGGTCAATGTGGTGTGGTGTGGTGTGGTGTG 900
781 ACCTACAGCTTGCAGCTGGGACATGAAGCAGGTCAATGTGGTGTGGTGTGGTGTGGTGTG 840
901 GTGGCTTGTGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
841 GTGGCTTGTGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
961 CATGAGGCGCATCCCATCTGCGACGGAACCTCATCTTCTTAGTGTGCCACTTGTCTTGGC 1020
901 CATGAGGCGCATCCCATCTGCGACGGAACCTCATCTTCTTAGTGTGCCACTTGTCTTGGC 960
1021 ATGGCTTCCACTGGGTCAACCACTTATCTATGGCTTCTCAACACCACTTCAAGAG 1080
961 ATGGCTTCCACTGGGTCAACCACTTATCTATGGCTTCTCAACACCACTTCAAGAG 1020
1081 GAGATCAAGGCGCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
1021 GAGATCAAGGCGCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
1141 CTGGCTTGTCCAGTACATACGAGTCTTCAAGGCTTCTTCAAGGCTTCTTCAAGGCTTCT 1200
1081 CTGGCTTGTCCAGTACATACGAGTCTTCAAGGCTTCTTCAAGGCTTCTTCAAGGCTTCT 1140
1201 TCCATCCCACTTAAACAGGCTTAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1240
1141 TCCATCCCACTTAAACAGGCTTAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1180

RESULT 6

US-08-495-695B-27

Sequence 27, Application US/08495695B
Patent No. 5976814
GENERAL INFORMATION:
APPLICANT: Bard, Jonathan A.
APPLICANT: Walker, Mary
APPLICANT: Branchek, Theresa
APPLICANT: Weinshank, Richard L.
TITLE OF INVENTION: DNA ENCODING A HUMAN NEUROPEPTIDE
Y/PEPTIDE YV/PANCREATIC POLYPEPTIDE
TITLE OF INVENTION: RECEPTOR (Y4) AND USES THEREOF
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/495,695B
FILING DATE: 13-Jan-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 44743-A-PCT-US/JPW/JHB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 1439 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 178..1306
US-08-495-695B-27

Query Match 61.4%; Score 810.8; DB 2; Length 1439;

Best Local Similarity 78.7%; Pred. No. 1.3e-194;

Matches 981; Conservative 0; Mismatches 262; Indels 3; Gaps 1;

QY	72	TCCTTTTCATCCACTATGAACACCTCTCACCTCTGCGCTTGTCTGCCAAATCTCC	131
Db	162	TCCTTTTCATCCACTATGAACACCTCTCACCTCTGCGCTTGTCTGCCAAATCTCC	221
QY	132	ACAAGGTGAACAGAGCAACCCCTGGGCAACCCATACAACTTCTCTGACATTTGCCA	191
Db	222	ACAAGGTGAACAGAGCAACCCCTGGGCAACCCATACAACTTCTCTGACATTTGCCA	281
QY	192	GGATTCCTGGAGGAGGATGCTTCATCGTCACCTTCTTACAGCATTTGAGACTGTGGG	251
Db	282	GGATTCCTGGAGGAGGATGCTTCATCGTCACCTTCTTACAGCATTTGAGACTGTGGG	341
QY	252	GTCTCTGGTAACTCTGCTGCTGATGTGTGACTGTGAGGAGAGAGGAGAGCAAGCT	311
Db	342	GTCTCTGGTAACTCTGCTGCTGATTTGTGACCAAGGAGAGAGGAGAGGAGTCAATGT	401
QY	312	GACCACTGCTTATGCGCACTCTCTGACTTCTCTGACTTCTCTGCTCTCTGCTGCA	371
Db	402	GACCACTGCTTATGCGCACTCTCTGACTTCTCTGACTTCTCTGCTCTCTGCTGCA	461
QY	372	GCGCTGACCGCGCTCTACACCATCATGACTACTTGTGAGAGAGCCCTCTGCA	431

Db 462 GCGCTCAGGTCACCTACACATCATGACTACTGGATCTTCGGGAGTCCCTTCCAA 521
Qy 432 GATGTCGGCCCTTATCCAGTGTGTGGTGAAGGTCCTCATCTCTCGCTCGCTCGT 491
Db 522 GATGTTAAAGTTCATCCAGTGTGTGGTGAAGGTCCTCATCTCTCGCTCGCTCGT 581
Qy 492 GGCCTCGAGAGGATCAGCTCATCAACCCCAAGGTCGGAAGCCAGCATCTCACA 551
Db 582 GGCCTCGAGAGGATCAGCTCATCAACCCCAAGGTCGGAAGCCAGCATCTCACA 641
Qy 552 GGCCTACCTGGGATGTGCTCATCTGGTCAATGCTGTGCTGTCTCTCTCTCTCT 611
Db 642 GGCCTACCTGGGATGTGCTCATCTGGTCAATGCTGTGCTGTCTCTCTCTCTCT 701
Qy 612 GGCCTACCTGGGATGTGCTCATCTGGTCAATGCTGTGCTGTCTCTCTCTCTCT 671
Db 702 GGCCTACCTGGGATGTGCTCATCTGGTCAATGCTGTGCTGTCTCTCTCTCTCT 761
Qy 672 GGCAGATAAGGTGTGCTGTACCGAGTCTCTGCGCACTGCTCACCACCGCATCTAC 731
Db 762 GGCAGATAAGGTGTGCTGTACCGAGTCTCTGCGCACTGCTCACCACCGCATCTAC 821
Qy 732 CACCTTCTGCT 791
Db 822 CACCTTCTGCT 881
Qy 792 AGCATCTACCGGCGCTCTGAGAGGAGGCGGCGCTGTTTACAGGCGCACTACAG 851
Db 882 GGTATCTATCAGCGCTCTGAGAGGAGGCGGCGCTGTTTACAGGCGCACTACAG 941
Qy 852 GCGAGCTGGGACATGAGAGGAGTCAATGTGTGTGTGTGTGTGTGTGTGTGTGT 911
Db 942 ACAGTGGGGAGATGAGAGGAGTCAATGTGTGTGTGTGTGTGTGTGTGTGTGT 1001
Qy 912 CGTGTCTGCTGCT 971
Db 1002 AGTTCCTGCTGCT 1061
Qy 972 CCCCCTGCGCAGGAGGAGTCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1031
Db 1062 CCCCCTGCGCAGGAGGAGTCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1121
Qy 1032 CTGCGTCAACCATTCATCTATGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1091
Db 1122 CTGCTCAACCATTCATCTATGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1181
Qy 1092 CTGCTGCTGCT 1151
Db 1182 TCTGCTCTGCT 1241
Qy 1152 CACAGTACATGAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1211
Db 1242 CACTGTGCACGAGGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1301
Qy 1212 TTAACAGGCTAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1271
Db 1302 GTAGTCACTCTAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1358
Qy 1272 GTGGGCACTGAGGCTGGGTCGACCGGAGGATCTCTCTCTCTCTCTCTCTCT 1317
Db 1359 GTAGACAAATGCAAGCTGTGTATCATCTCTCTCTCTCTCTCTCTCTCTCTCT 1404

RESULT 7

PCT-US94-14436-27
; Sequence 27, Application PC/TUS9414436
; GENERAL INFORMATION:
; APPLICANT: Bard, Jonathan A.
; APPLICANT: Walker, Mary
; APPLICANT: Branchek, Theresa
; APPLICANT: Weinshank, Richard L.
; TITLE OF INVENTION: DNA ENCODING A HUMAN NEUROPEPTIDE

; TITLE OF INVENTION: Y/PEPTIDE YY/PANCREATIC POLYPEPTIDE
; TITLE OF INVENTION: RECEPTOR (Y4) AND USES THEREOF
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/14436
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44743-A-PCT\JPW\MAT
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1439 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 178..1306
; PCT-US94-14436-27

Query Match 61.4%; Score 810.8; DB 5; Length 1439;
Best Local Similarity 78.7%; Pred. No. 1.3e-194;
Matches 981; Conservative 0; Mismatches 262; Indels 3; Gaps 1;
Qy 72 TCTTTTACATCATGACACCTCTCAGCTCTCGCTTCTGCTCCCAAAATCTCC 131
Db 162 TCTTCTCACACCAACATGATACCTCTATCTATGAGCTCCCTTCTCCGCGATCTCT 221
Qy 132 ACAAGGTGAAAACAGAGCAAAACCCCTGGGCAACCCCATACAACTTCTGTGAACATGGCCA 191
Db 222 ACAAGGTGAAAATGGGACCAACCCACTGGATTCCTCTATAATCTCTGACGGCTGCCA 281
Qy 192 GGATTCGGTGGAGCTGATGCTTCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 251
Db 282 GGATTCGGGAGATCTGTGTGGCTTCTATCATCTACCTACAGCTTGAGACCTCTTGGG 341
Qy 252 GGCTCTGGGTAACTCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 311
Db 342 GGCTCTAGGAAACCTCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 401
Qy 312 GACCAACCTCTTATGCGCAACCTGGCTTCTCTGACTTCTCTCTCTCTCTCTCTCTCTG 371
Db 402 GACCAACCTCTTATGCGCAACCTGGCTTCTCTGACTTCTCTCTCTCTCTCTCTCTCTG 461
Qy 372 GCGCTGACCGCGCTCTACACCATCTGACTTCTGATCTTTGGAGAGACCTCTGCAA 431
Db 462 GCGCTCACGGTCACCTTACACCATCTGACTTCTGATCTTCGGGAGTCTCTTGGCAA 521
Qy 432 GATGTCGGCTTCTATCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 491
Db 522 GATGTTAAAGTTCATCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 581
Qy 492 GGCCTCGAGAGGATCAGCTCATCAACCCCAAGGTCGGAAGCCAGCATCTCACA 551

[illegible]

RESULT a

US-08-415-818-5
Sequence 5, Application US/08415818
Patent No. 5621079
GENERAL INFORMATION:
APPLICANT: Cascieri, Margaret A.
APPLICANT: Linemeyer, David L.
APPLICANT: MacNeill, Douglas J.
APPLICANT: Shiao, Lin-Lin
APPLICANT: Strader, Catherine D.
APPLICANT: Tan, Carina P.
APPLICANT: Weinberg, David H.
TITLE OF INVENTION: NEUROPEPTIDE Y RECEPTOR
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mary A. Appollina
STREET: P.O. Box 2000, 126 E. Lincoln Ave.

501	QY	GAGGCATCAGCTCATCATCAACCCACAGAGCTGGAGCCACAGCATCTCAGAGCGCTACCT	560
1220	Db	ACGATATCAGCTGATTGTGAACCCCGCTGGCTGGAAACCCAGAGTAGCTCATGCCATTG	1279
561	QY	GGGATTGTGCTCATCTGGGTTCATTGCTGTGCTCTCTCCCTGCCCTTCCTGGCCACAG	620
1280	Db	GGGATCATCTTGATTGGCTCATTTCTCTGACATCTCTATTCCCTTATTCCTGTCTTA	1339
621	QY	CATCCTGGAGAAATGCTTTCCACAGAACCACTCCAAGGCTCTCGAGTTCCTGGCAGATAA	680
1340	Db	CCACCTCACCAAATGAGCGCTTTTCATAATCTCTCTCTCCCTACTGACATCTACACCCACCA	1399
681	QY	GGTGGTCTGTACCGAGTCCCTGGCCACTGGCTCACACCGCACCATCTACACCACTTCCT	740
1400	Db	GGTAGCTTGTGTGAGATTGGCCCTTCTAACTGAACAACTCCTCTTTCTTCTACATCAT	1459
741	QY	GCTCCTCTTCCAGTACTCCCTCCCACTGGGCTTCATCTGGCTGTGTTATGCAAGCATCTA	800
1460	Db	ATTATATGCTCCAGTATTTGTGCTCTCTGGGTTTCATTCTTATCTGTACCTGAAGATCGT	1519
801	QY	CCGGCGCTGCAGAGGACAGGGCGCGTGTTCACAAGGGACCTTACAGCTTG---CGAGC	857
1520	Db	TCTCTGCTCTCGAAAAAGAACTAGCGAGGTGGACAGGAGAAAGAAATAAGAGCCGTCT	1579
858	QY	TGGGCACATGAAGCAGGTCAATGTGTGTGCTGGTGTATGGTGTGGCTTTTGGCGTGTCT	917
1580	Db	CAATGAGAACAAAGAGGTAAATGTGATTTCATCGTAGCTGACTTTTGGAGCGTG	1639
918	QY	CTGGCTGGCTCTGCATGTGTTCAACAGCCTGGAAGACTGGCACCATCAGAGCCATCCCAT	977
1640	Db	CTGGTGGCCCTTGAACATTTTCAATGTCACTTCGACTGGTATCATGAGATGCTGATGAG	1699
978	QY	CTGCAAGGGAACCTCATCTTCTTAGTGTGCCATCTGCTGCCATGGCTTCCACCTCGGT	1037
1700	Db	CTGCCACCAAGACCTGTGATTTGTAGTTTGGCACTTGATTCGTATGGTTTCTACTTCGAT	1759
1038	QY	CAACCCCATTCATCTATGGCTTTCTACACCACTTCACAAGGAGATCAAGGGCCCTGGT	1097
1760	Db	AAATCTCTCTTTTATGSAATTCTCAACAAAACCTTCACAAGGATCTTAATGATGCTTAT	1819
1098	QY	GCTGACTTGGCCAGCAGACGCCCCCTGGAGGAGTTCGGAGCATCTGCCCTGTCCACAGT	1157
1820	Db	TCACCATGTGTGGTGTGGTGAACCTCAGAAAGTTATGMAAATATTGCCATGCTACTAT	1879
1158	QY	ACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGGTCCAAATCCCAATTA	1214
1880	Db	GCAACAGATGAATCCCAAGGATCATTAATAACTGGCTCACATACCAACAGAGCATATA	1936

RESULT 9

US-08-894-326-5
 ; Sequence 5, Application US/08894236
 ; Patent No. 5939263
 ; GENERAL INFORMATION:
 ; APPLICANT: Cascieri, Margaret A.
 ; APPLICANT: Lineneyer, David L.
 ; APPLICANT: MacNeil, Douglas J.
 ; APPLICANT: Shiao, Lin-Lin
 ; APPLICANT: Strader, Catherine D.
 ; APPLICANT: Tan, Carina P.
 ; APPLICANT: Weinberg, David H.
 ; TITLE OF INVENTION: NEUROPEPTIDE Y RECEPTOR
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Mary A. Appollina
 ; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
 ; CITY: Rahway
 ; STATE: NJ
 ; COUNTRY: USA
 ; ZIP: 07065
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION INFORMATION:
; APPLICATION NUMBER: US/08/894,236
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/383,746
; FILING DATE: 03-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/415,818
; FILING DATE: 03-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Appollina, Mary A.
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19390Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508-594-3462
; TELEFAX: 508-594-4720
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2280 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 822..1937
; US-08-894-236-5

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Query Match	21.1%	Score 278.6	DB 2	Length 2280
Best Local Similarity	53.2%	Pred. No. 1.4e-60		
Matches 637	Conservative 0	Mismatches 554	Indels 6	Gaps 2
Qy	24	GTAGGGCGTCATCCCTCAAGTGTATCACTTAGTTTCAAGAGTCCTGGGAATCTTTTACATC 83		
Db	740	GTGTGCTCTCAGAGCAACATGGCCAAACATCCACTGAGGATACAGGAGCTTAGAATAAT 799		
Qy	84	CACATATGAACACCTCTCACCTCTCTGGCTTGTCTGCTCCCAAAATCTCCACAAGGTGAAAA 143		
Db	800	CTCTAATTAATAATCTTGACATAATGGAAGTGCTCACAAAACAGGCCAACACCTAATAAACC 859		
Qy	144	CAGAGCAAAACCCCTGGGACCCCATACAACTTCTTGAAATTTGCACAGGATTCGGTGGGA 203		
Db	860	CAGTGGCAAGAGCAACAACCTCGGCATTTTCTACTTTGAATCTCTGCCAAACCCCTTTTCT 919		
Qy	204	CGTGATGGTCTTCATCGTGTCACTTCTACAGCATTTGAGACTGTCTGTGGGGTCTGGGGTAA 263		
Db	920	AGCCATTAATCTTGCTACTCTTAGCATATATCTGTGATCCTTAATCATGGGCATTTTGGAAA 979		
Qy	264	CCTCTGCTGATGTGTGTGATGTGTGAGGCAGAGGAGAAAGCC---AACGTGACCAACCT 320		
Db	980	CCTCTCTTTATCATCATCATCTTTAAGAAACAGAGAGAGCTCAAATGTTACCAACAT 1039		
Qy	321	GCTTATCGCCAAACCTGGCCCTTCTTGACTTCTCATGTGCTCTCTCTGCGACGCGCTGAC 380		
Db	1040	ACTGAATGCCAAACCTGTCCCTCTCTGACATCTTGGTGTGTGTCATGTGCATCCCTTTTAC 1099		
Qy	381	CGCGCTCTACACCATCATGGACACTCGATCTTTGGAGAGACCCCTCTGCAAGATGTGGCC 440		
Db	1100	GGTCATCTACACTCTGATGGACCACTGGGTATTTGGGAAACACTATGTGTAACCTCACATTC 1159		
Qy	441	CTTCATCCAGTGTGTCGGTGAAGCGTCTCCATCCTCTCGCTCTCTCTCGTGGGCCCTGGA 500		
Db	1160	CTAGTGCAAGTGTCTCAGTTTCTGTGTCCATATCTCCCTCTGTGTTGATTGCTATTGA 1219		
Qy	501	GAGGCATCAGCTCATCATCAACCAACAGGCTGGAAGCCCGACATCTCACAGGCGCTACCT 560		
Db	1220	ACGATATCAGCTGATTTGAACCCCGTGGCTGGAAACCCAGAGTAGCTCATGCTCATTTG 1279		

Db 1051 GCTGATGAGCTGCCACACGACCTGGTATTTGTATTTGGTTCACCTGGTGTCTATGGTTTC 1110
QY 1029 CACCTGCGCTCAACCAATTCATCTATGGCTTTCTCAACACCACTTCAAGAGGAGATCAA 1088
Db 1111 CACATGTATAACCTCTCTTTATGGCTTTCTCAGCAAAATTTCCAAAGGACCTGGT 1170
QY 1089 GGCCTGTGTGACTTGGCCAGCAGAGCGCCGCCCTGTGGAGAGTCGGAGCATCTGCCCT 1148
Db 1171 AGTGTATTACCACTGCTGTGTCTTCCACACCTCAGGAAAGATGTGAAATATTGGCAT 1230
QY 1149 GTCCACAGTACATACGGA 1166
Db 1231 CTCCACTATGCACACAGA 1248

RESULT 13

PCT-US96-01444-11
; Sequence 11, Application PC/ITUS9601444
; GENERAL INFORMATION:
; APPLICANT: Cascieri, Margaret A.
; APPLICANT: Linemeyer, David L.
; APPLICANT: MacNeill, Douglas J.
; APPLICANT: Shiao, Lin-Lin
; APPLICANT: Strader, Catherine D.
; APPLICANT: Tan, Carina P.
; APPLICANT: Weinberg, David H.
; TITLE OF INVENTION: NEUROPEPTIDE Y RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mary A. Appollina
; STREET: P. O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/01444
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/383,746
; FILING DATE: 03-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/415,818
; FILING DATE: 03-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Appollina, Mary A.
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19390Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-594-3462
; TELEFAX: 908-594-4720
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1499 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: gDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
PCT-US96-01444-11

Query Match 20.2%; Score 266; DB 5; Length 1499;

Best Local Similarity 53.9%; Pred. No. 1.8e-57;

Matches 592; Conservative 0; Mismatches 500; Indels 6; Gaps 2;

QY 75 TTTCATCCACTATGAACACCTCTCACCTCTGGCTGTGTCTTCCCAAAATCTCCACA 134

Db 151 TTAGAAATCTCTTCTTACAACTCTGACAAATGGAAGTTTCCCTAAACACCCAGCATC 210
QY 135 AGGTGAAAAACAGAAACCCCTGGGACCCCATACAACTTCTCTGAACATTTGCCAGGA 194
Db 211 TAATACACAGCACAAGAAACAACACTCGCAATTTTCTTACTTTAGTCTCTGCAACC 270
QY 195 TTCCGTGGAGTGAAGTCTTCACTCTTCACTTCTTACAGCATTTGAGACTGTGCGTGGGGT 254
Db 271 CCCTTCTCCAGCTTTACTCTTATATGATAGCTATCTGTGGTCTTAAATTTGTGGGCT 330
QY 255 CTTGGGTAACTCTGCTGCTGATGTGTGACTGTGAGGCAAGAGGAGAAAGC---CAACGT 311
Db 331 TTTTGGAAACCTCTCTCTCATCATCATCATCTTTAAGAGCAGAGAAAGCTCAGAAAT 390
QY 312 GACCAACCTGCTTATGCGCAACCTGGCCCTTCTGTGACTTCTCAATGTGCTCTCTGCGCA 371
Db 391 CACGACATACCTGATGCGCAATCTCTCCCTCTCTGATACCTTGGTGTGTGATGTCAT 450
QY 372 GCGCTGACCGGCTCTACACCATCATGACTACTGTGATCTTTGGAGAGACCTCTGCAA 431
Db 451 CCAATTTACTATCATCTACACTCTGATGACCACTGATTTGGGATACCATGTGCGAG 510
QY 432 GATGCGGCTTCACTCAGTGTGATGTGCGTGTCTCCATCTCTCTCTCTCTCTCTCTCT 491
Db 511 ACTCACATCTATGTGAGAGTGTCTCAATCTCTGTGTCCATATCTCACTTGTATTCAC 570
QY 492 GCGCTGGAGAGCATCAGCTCATCAACCCACAGAGCTGGAGCCAGCCAGCATCTCACA 551
Db 571 TGCTGTGAAAGATATCAGCTAATTTGTGAACCCCTGCTGGAGCCAGCCAGTGTGACT 630
QY 552 GGCCTACTCTGGGATTTGCTCATCTGTGGTGTCTTGTCTCTCTCTCTCTCTCTCTCT 611
Db 631 TGCTTACTGGGCACTCACACTGATTTGGTGTCTTCTCTCTCTCTCTCTCTCTCTCT 690
QY 612 GGCACACAGCATCTCGAAGATGTCTTCCAGAAACCACTCAAGGCTCTGGAGTCTCT 671
Db 691 CTTGCTCTACCACTCTCAGTGTGAGCTTCTCCACACCTCTCTCTCCCACTGACTCTA 750
QY 672 GGCAGATAAGTGTGTCTGACGAGTCTGGGCACTGGCTCACCACCGACCATCTACAC 731
Db 751 CACCCACAGTGTGCTGTGGAGACTGGCCCTCCAAAGAGCCGCTGCTCTCTCAC 810
QY 732 CACCTTCTGCTCTCTTCTCAGTGTCTCTCAGTGTCTCTCAGTGTCTCTCTCTCTCT 791
Db 811 CACCT 870
QY 792 ACGCATCTACCGCGCTCTCAGAGGCGGGCGGTCTTCAAGGGCACTCTACAGCTT 851
Db 871 GAAGATTGTATCTGCTCGCAGAGAAATGCAAGGTAGATAGAGAGGAAATGA 930
QY 852 G---CGAGCTGGSCACATGAAGCAGGTCAATGTGGTGTCTGGTGTGATGGTGGCTTT 908
Db 931 GGGCCGCTCAATGAGAAACAAGAGGATCAACAATGTTGATTTCCATCGTGGTACCTT 990
QY 909 TGCCGTGCTCTGGCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTG 968
Db 991 TGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1050
QY 969 CATCCCCATCTGCCACGGAACTCTCTTCTTGTGTGCTCTCTCTCTCTCTCTCTCTCT 1028
Db 1051 GCTGATGAGCTGCCACCAAGCCTGTGATTTGTAGTTTGGCACTTGGTGTGCTGCTTTC 1110
QY 1029 CACCTGGTCAACCCATTCATCTATGGCTTCTCAACACCACTTCAAGAGGAGATCAA 1088
Db 1111 CACATGTATAAACCTCTCTTTATGGCTTCTCAACAAAAATTTCCAAAGAGACCTGGT 1170
QY 1089 GGCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1148
Db 1171 AGTGCTTATTCACCACTGCTGCTGCTTCACTCTCAGGAAAGATGTGAAATATTGCCAT 1230
QY 1149 GTCCACAGTACATACGGA 1166

Db	1231	CTCCACTATGCACACAGA	1248
RESULT 14			
US-09-045-186-1			
; Sequence 1, Application US/09045186			
; Patent No. 6087154			
; GENERAL INFORMATION:			
; APPLICANT: Baez, Melvyn			
; APPLICANT: Cates, Carolyn A.			
; TITLE OF INVENTION: RHESUS NEUROPEPTIDE Y1 RECEPTOR			
; NUMBER OF SEQUENCES: 3			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Eli Lilly and Company			
; STREET: Lilly Corporate Center			
; CITY: Indianapolis			
; STATE: Indiana			
; COUNTRY: United States of America			
; ZIP: 46285			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Patent In Release #1.0, Version #1.30			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/09/045,186			
; FILING DATE:			
; CLASSIFICATION:			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Gaylo, Paul J.			
; REGISTRATION NUMBER: 36,808			
; REFERENCE/DOCKET NUMBER: P-11376			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (317) 276-0756			
; TELEFAX: (317) 276-3861			
; INFORMATION FOR SEQ ID NO: 1:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 1152 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
; MOLECULE TYPE: cDNA			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: 1..1152			
; US-09-045-186-1			
Query Match 19.5%; Score 257.6; DB 3; Length 1152;			
Best Local Similarity 55.0%; Pred. No. 2e-55;			
Matches 576; Conservative 0; Mismatches 459; Indels 13; Gaps 3;			
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Dd	210	GATGAGAATGTATACCAACATCTGATGTGACCTTTCTTCACAGACTTGTCTGCG	269
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QY	480	GCTCGCTCCTGCTGGCCCTGGAGGAGCATCAGCTCATCATCAACCAACAGAGCTGGAAGCC	539

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/ / APPLICATION NUMBER:  US/09/045,186-3
/ /
/ / FILING DATE:
/ /
/ / CLASSIFICATION:
/ /
/ / ATTORNEY/AGENT INFORMATION:
/ /
/ /   NAME:  Gaylo, Paul J.
/ /
/ /   REGISTRATION NUMBER:  36,808
/ /   REFERENCE/DOCKET NUMBER:  P-11376
/ /
/ / TELECOMMUNICATION INFORMATION:
/ /
/ /   TELEPHONE:  (317) 276-0756
/ /   TELEFAX:  (317) 276-3861
/ /
/ /   INFORMATION FOR SEQ ID NO:  3 :
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/ /     LENGTH:  152 base pairs
/ /     TYPE:  nucleic acid
/ /     STRANDEDNESS:  single
/ /     TOPOLOGY:  linear
/ /
/ /     MOLECULE TYPE:  mRNA
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/ /   US-09-045-186-3

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Search completed: May 11, 2004, 12:30:58
Job time : 121 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 10, 2004, 22:22:56 ; Search time 582 Seconds
(without alignments)
10274.207 Million cell updates/sec

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Perfect score: 1320
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2941586 seqs, 2264995651 residues

Total number of hits satisfying chosen parameters: 5883172

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:
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3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
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19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1210	91.7	1959	9	US-09-864-761-4424
2	1180	89.4	1180	16	Sequence 4424, Ap
3	1128	85.5	1128	15	Sequence 1061, Ap
4	1128	85.5	1128	15	Sequence 11, Appl
5	959.4	72.7	983	9	Sequence 202, App
6	569.2	43.1	581	15	Sequence 21172, A
7	278.6	21.1	2281	9	Sequence 12634, A
8	257.6	19.5	1155	15	Sequence 1, Appli
9	257.6	19.5	1155	15	Sequence 9, Appli
10	257.6	19.5	1605	9	Sequence 9, Appli
11	257.6	19.5	1605	12	Sequence 1, Appli
12	257.6	19.5	1605	15	Sequence 3, Appli
13	257.6	19.5	1605	15	Sequence 1, Appli
14	257.6	19.5	1605	15	Sequence 3, Appli

15	257.6	19.5	1605	15	US-10-291-446-1	Sequence 1, Appli
16	257.6	19.5	1605	16	US-10-305-720-1231	Sequence 1231, Ap
17	257.6	19.5	1888	15	US-10-176-847-25	Sequence 25, Appl
18	257.6	19.5	2624	15	US-10-017-273A-2	Sequence 2, Appli
19	257.6	19.5	2752	13	US-10-342-887-538	Sequence 538, App
20	257.6	19.5	2752	13	US-10-172-118-538	Sequence 538, App
21	257.6	19.5	2752	15	US-10-225-567A-377	Sequence 377, App
22	257.6	19.5	2752	15	US-10-177-293-329	Sequence 329, App
23	257.6	19.5	2752	16	US-10-295-027-639	Sequence 639, App
24	257.6	19.5	2752	16	US-10-295-027-745	Sequence 745, App
25	257.6	19.5	3210	15	US-10-198-846-11438	Sequence 11438, A
26	255.6	19.4	1957	15	US-10-225-567A-375	Sequence 375, App
27	255.6	19.4	1957	16	US-10-305-720-1169	Sequence 1169, Ap
28	254	19.2	1952	13	US-10-181-906-15	Sequence 15, Appl
29	253.8	19.2	1401	13	US-10-181-906-5	Sequence 5, Appli
30	156	11.8	1110	14	US-10-044-592-17	Sequence 17, Appl
31	156	11.8	1110	15	US-10-251-385-177	Sequence 177, App
32	156	11.8	1110	15	US-10-278-087A-31	Sequence 31, Appl
33	156	11.8	1113	15	US-10-225-567A-244	Sequence 244, App
34	154.4	11.7	1331	14	US-10-044-592-73	Sequence 73, Appl
35	152.8	11.6	1110	15	US-10-251-385-25	Sequence 25, Appl
36	152.8	11.6	1335	16	US-10-305-720-1051	Sequence 1051, Ap
37	146	11.1	146	15	US-10-029-386-26334	Sequence 26334, A
38	138.2	10.5	1293	9	US-09-866-248A-7	Sequence 7, Appli
39	138.2	10.5	1293	15	US-10-225-567A-657	Sequence 657, App
40	131.8	10.0	1320	9	US-09-292-973-3	Sequence 3, Appli
41	128.2	9.7	1200	15	US-10-017-273A-3	Sequence 3, Appli
42	128.2	9.7	1200	16	US-10-366-288-37	Sequence 37, Appl
43	128.2	9.7	1200	16	US-10-305-720-1062	Sequence 1062, Ap
44	128.2	9.7	1280	15	US-10-188-619-1	Sequence 1, Appli
45	128.2	9.7	3241	13	US-10-181-906-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-864-761-4424
; Sequence 4424, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663


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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
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; SEQ ID NO 4424
; LENGTH: 1959
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006184.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.94
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
; NAME/KEY: unsure
; LOCATION: 445
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Qy 121 CCAAAATCTCCAAAGTGTAAAAAGCAAGCAAAACCCCTGGGCAACCCCATCAAACTTCTCT 180
Db 207 CCAAAATCTCCAAAGTGTAAAAAGCAAGCAAAACCCCTGGGCAACCCCATCAAACTTCTCT 266
Qy 181 GAACATGCCAGGATTCGTTGGAGTGTGTTCTTCATGTCACCTTCTCTACAGCATTGAG 240

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Qy	328	GCCAACTGGCCCTTCCTGTGACTTCCTCATGTGCTCTCTGTGCCAGCCGCTGACCGCGCTC	387
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Qy	448	CAGTGCATGTGCGTGAGCGGTCTCCATCTCTCGTCTGCTCTGTGCGCCCTGGAGAGGCAT	507
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Qy	688	TGTACCGAGTCTGGCCACTGGGTCAACACCGACCACTACACCACTTCCTGCTGCTCTC	747
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US-10-225-567A-202
; Sequence 202, Application US/10225567A
; Publication No. US20030113798A1


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; FILE REFERENCE: R-639
; CURRENT APPLICATION NUMBER: US/09/900,497
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US 60/216,260
; PRIOR FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: US 60/221,474
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
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; ORGANISM: Mus musculus
US-09-900-497-1

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Best Local Similarity 53.2%; Pred. No. 2.2e-70;
Matches 637; Conservative 0; Mismatches 554; Indels 6; Gaps 2;

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DB 861 CAGTGGCAAGCAACAACCTCGGATTTTCTACTTTGAATCTCGCAACCCCTTTTCT 920
QY 204 CGTATGTCTTCATCGTCACTCTCTACAGCATGAGACTCTCGTGGGGTCTCGGTAA 263
DB 921 AGCCATCTCTTGCTACTATAGCATATACCTGTGATCTTAATCATGGCACTTTTGGAA 980
QY 264 CTTCTGCTGTGATGTGATGTGAGCTGTGAGCAGAGAGAAACC---AACGTGACCACT 320
DB 981 CCTCTCTTATCATCATCATCTTTAAGAAACAGAGAGAACTCAAAATGTTACCAACAT 1040
QY 321 GCTATGCCAACCTGGCTCTCTGACTTCTCTATGCTCTCTCTGCGAGCGCTGAC 380
DB 1041 ACTGATGCCAACCTGGCTCTCTGACTTCTCTATGCTCTCTCTGCGAGCGCTGAC 1100
QY 381 CGCGCTCTACACCATCATGAGTACTGTGATCTTTGGAGAGACCTCTGCAAGATGTGGC 440
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QY 441 CTTATCCAGTGCATGTCTGCTGAGCTCTCATCTCTCTGCTCTGCTCTGCTGCGCTGGA 500
DB 1161 CTAGTGCAAGTGTCTCAGTTCTGTGTCCATATCTCCCTGTGTGTGATGTCTATGA 1220
QY 501 GAGGCATCAGTCTCATCAACCCAGGCTGGAAGCCAGCATCTCACAGGCTTACCT 560
DB 1221 ACGATATCAGCTGATGTGAACCCCGGTGGTGGAAACCCAGAGTAGCTCATGCTATTG 1280
QY 561 GGGGATCTGCTCATCTGGGTCACTGCTGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 620
DB 1281 GGGGATCACTGTGATTTGGCTCACTTCTCTGACATGTCTATTCCCTTATTCCTGTGCTTA 1340
QY 621 CATCTGGAGATGTCTTCCAAAGAACCACTTCAAGGCTCTGGAGTTCCTGGCAGATAA 680
DB 1341 CCACCTCAACCAATGAGCCCTTTCATAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1400
QY 681 GGTGCTGTACCGAGTCTCTGGCACTGGCTCACCACCGCACCATCTACACCACTTCTCT 740
DB 1401 GGTAGCTGTGTGGAGATTTGGCTTCTTAAACTGAACCACTCTCTCTCTCTCTCTCTCT 1460
QY 741 GCTCTCTTCCAGTACTGCTCCCACTGGGCTTATCTCTGCTGTGTGTATGACCGCATCTA 800
DB 1461 ATTTATGCTCCAGTATTTTGGCTCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1520
QY 801 CCGGCGCTTGAGAGGAGGGGGGTGTTTCAAGGGCACTTACAGCTTG---CGAGC 857
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RESULT 8

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US-10-309-515-9
; Sequence 9, Application US/10309515
; Publication No. US20030114644A1
; GENERAL INFORMATION:
; APPLICANT: Bennett Kinkade, Michele
; APPLICANT: Brodbeck, Robbin M.
; APPLICANT: Waters, Stephen E.
; APPLICANT: Krause, James E.
; TITLE OF INVENTION: Melanin Concentrating Hormone Receptors
; CURRENT APPLICATION NUMBER: US/10/309,515
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/284,835
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: 10/126,764
; PRIOR FILING DATE: 2002-04-18
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 1155
; TYPE: DNA
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US-10-309-515-9
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Query Match      19.5%; Score 257.6; DB 15; Length 1155;
Best Local Similarity 55.0%; Pred. No. 2.2e-64;
Matches 576; Conservative 0; Mismatches 459; Indels 13; Gaps 3;

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DB 150 GATCATCTTGTGTCTCTGGAAACTGTCCTTGTATCATATCATCTTGAACAAAGGA 209
QY 300 GAAAGCAACGTGACCAACTCTCTTATGCCAACCTGGCCCTTCTCTGACTTCTCATGTG 359
DB 210 GATGAGAAATGTTACCAACATCTGATGTGAACCTTTCTCTCTCAGACTTGTCTTGTGC 269
QY 360 CTTCTCTGCCAGCGCTGACCGCTCTACACCATCATGAGTACTGTGACTCTTGTGAGA 419
DB 270 CATCATGTCTCTCCCTTTTACATTTGTCTPACACATTAATGGACCACCTGGGTCTTGTG 329
QY 420 GACCTCTCTCAAGATGTCTGGCCCTTTCATCCAGTGCATGTCTGGTGAOCTCTCCATCTCTC 479
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330 GCGCATGTGAAGTTGAATCCTTTTGTGCAATGTGTTTCAATCAGTGTGCTTCTC 389
480 GCTGCTCCTCGTGGCCCTGAGAGGATCAGCTCATCATCAACCCACAGGCTGGAAGCC 539
390 TCTGGTCTCATGCTGTGGAACACATCAGCTGATTAATCAACCCCTGAGGGTGAAGCC 449
540 CAGCATCTCAGAGCCCTACCTGGGGATGTGCTCATCTGGGTCAATGCTGCTCTC 599
450 AATAATAGACATGCTTATGTAGTATGCTGTGATTTGGTCTTGTGCTGCTTCTC 509
600 CTTGCCCTCTCTGCGACAGCATCTGAGAGATCTTCCAGAGATGTCTTCCAGAGCC 659
510 TTTGCCCTCTCTGAGTATCAACAGTAATGACTGATG-----AGCCGTTCCAAATGTAAC 563
660 TCTGGAGTCTCTGCGACAGTAAGTGTGCTGTACCGAGTCTCTGCGCACTGCTCACCACCG 719
564 ACTTGATGCTGACAAAGACAAATACGTTGCTTTGATCAATTTCCATCGACTCTCATAG 623
720 CACCATCTACAGCACTCTCTGCTCTCTTCCAGTACTGCTGCTGCTGCTGCTGCTGCT 779
624 GTTGTCTTATACCACTCTCTCTTCTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCT 683
780 GGTCTGTATGACAGCATCTACCGGCGCTGACAGAGCAGGGGGGCTGTTTCCACAA--- 836
584 TATTTGCTACTTCAAGATATATACGCTTAAAGAGAGAAACAAATGATGACAGAT 743
837 GGGCACTCAGAGCTGCGAGCTGGGACATGAAGCAGGTCAATGTGCTGCTGCTGCTGCT 896
744 GAGAGACAATAAGTACAGGCTCAGTGAACCAAAAGAAATCAATATCATGCTGCTCCAT 803
897 GGTGGTGGCTTTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 956
804 TGTGTTAGCAATTTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 863
957 GCACCATGAGCCATCCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1016
864 GAATCATCAGATCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 923
1017 TGCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1076
924 AGCAATGATATCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 983
1077 GAAGAGATCAAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1136
984 GAGAGACTTGCACTTCTTCTTCAACTTTTGTGATTTCCGGTCTCGGATGATGATTATGA 1043

RESULT 9

US-10-126-764-9
; Sequence 9, Application US/10126764
; Publication No. US20030166834A1
; GENERAL INFORMATION:
; APPLICANT: Bennett Kinrade, Michele
; APPLICANT: Brodbeck, Robbin
; APPLICANT: Krause, James
; TITLE OF INVENTION: MELANIN CONCENTRATING HORMONE RECEPTORS
; FILE REFERENCE: NO. 2102
; CURRENT APPLICATION NUMBER: US/10/126,764
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: 60/284,835
; PRIOR FILING DATE: 2001-04-19
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9

; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-126-764-9
Query Match 19.5%; Score 257.6; DB 15; Length 1155;
Best Local Similarity 55.0%; Pred. No. 2.2e-64;
Matches 576; Conservative 0; Mismatches 459; Indels 13; Gaps 3;
180 TGAACATGCCAGGATTCGGTGGAGGTGATGCTTCAATGCTCACTTCTCTCAGCATGA 239
90 TGATGATTTGTCATCTGCCCTTTGGCCATGATATTTACCTTAGCTTCTTGGAGCTGT 149
240 GACTCTCGTGGGGTCTCGGTAACTCTGCTCATGTGTGCTGCTGAGCGCAGAGGA 299
150 GATCATTTCTGGTGTCTCTGGAACCTTGGCTTGTATCATATCATCTTGAACAAAGGA 209
300 GAAAGCCAAAGTGAACCACTGCTTATCGCCAACTGGGCTTCTCTGACTTCTCTCATGTG 359
210 GATGAGAAATGTATACCAACATCTCTGATTTGAACCTTCTCTCTCAGACTTGTCTTGC 269
360 CCTCTCTGCGCAGCGCTGAGCGGCTCTACCATCATGCACTACTGATGATCTTTGGAGA 419
270 CATCATGTGTCTCCCTTTATATTGCTACATTAATGATGACCACTGGTCTTTGGTGA 329
420 GACCTCTGCAAGATGTGCGCTTTCATCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 479
330 GCGCATGTGTAAAGTTGAATCTTTTGTGCAATGCTTTTCAATCACTGCTGCTCAATTTCTC 389
480 GCTCTCTCTGCGGCTGAGAGGATCACTCATCATCAACCCACAGGCTGGAAGCC 539
390 TCTGTTCTCATGCTGTGGAACGACATCAGCTGATATCAACCTCGAGGTGGAAGCC 449
540 CAGCATCTCAGAGGCTTACCTGGGATTTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCT 599
450 AATAATAGACATGCTTATGTAGTATTTGCTGATTTGGTCTGCTGCTGCTGCTGCTGCT 509
600 CTTGCCCTTTCTGCGCAACAGCTCTTGGGAAATGCTTCCACAGAACCACTCCAAGCC 659
510 TTTGCTTTCTGATCTACCAAGTAAAGCTGATG-----AGCGTTTCCAAATGTAAC 563
660 TGTGAGTCTCTGCGAGATAAGGTGCTGTACCGAGTCTCTGGCAGCTGCTGCTGCTGCTGCT 719
564 ACTGATGCTGACAAAGACAAATACGCTGCTTTGATCAATTTCCATCGGACTCTCATAG 623
720 CACCATCTACAGCACTTCTCTGCTCTTCCAGTACTGCTTCCACTGGGCTTCACTCT 779
624 GTTGTCTTATACCACTCTCTCTTGGTGTGCTGCTGCTTGGTCCACTTTTGTATATAT 683
780 GGTCTGTTTATGCAAGCATCTACCGGCTCTGAGAGCGAGGGGCGGTGTTTCAAA--- 836
584 TATTTGCTACTTCAAGATATATATAGCCCTAAAGAGAGAAACAAATGATGGAAGAT 743
837 GGGCACTCAGAGCTTGGAGTGGGACATGAAGCAGGTCAATGTGCTGCTGCTGCTGCTGCT 896
744 GAGAGACAATAAGTACAGGCTCCAGTGAACCAAAAGAAATCAATATCATGCTGCTCCAT 803
897 GGTGGTGGCTTTTGGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 956
804 TGTGTTAGCAATTTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 863
957 GCACCATGAGCCATCCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1016
864 GAATCATCAGATCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 923
1017 TGCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1076
924 AGCAATGATATCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 983
1077 GAAGAGATCAAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1136
984 GAGAGACTTGCACTTCTTCTTCAACTTTTGTGATTTCCGGTCTCGGATGATGATTATGA 1043

QY 1137 GCATCTGCCCTGTCCACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGG 1196
Db 1044 AACAAATAGCCATGTCCACAGTACACAGATGTTTCCAAAACCTCTTTGAAGCAA-----G 1099
QY 1197 CAGTCCCAATCCCAATTTAAACAGGTCTA 1224
Db 1100 CAAGCCAGTCGCATTTAAAAAATCAA 1127

RESULT 10
US-09-771-956-1
; Sequence 1, Application US/09771956
; Patent No. US2001003147A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Michele
; APPLICANT: Brobeck, Robin
; APPLICANT: Krause, James
; TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors
; FILE REFERENCE: N2000.001
; CURRENT APPLICATION NUMBER: US/09/771.956
; CURRENT FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1605
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-771-956-1

Query Match 19.5%; Score 257.6; DB 9; Length 1605;
Best Local Similarity 55.0%; Pred. No. 2.5e-64;
Matches 576; Conservative 0; Mismatches 459; Indels 13; Gaps 3;

QY 180 TGAACATTCGCCAGGATTCGGTGGACGTGATGTTCTCATGTCACCTTCTTACAGCATTA 239
Db 286 TGAATGATGTCATCTGCCCTTGGCCATGATATTTACTTAGCTTGTCTATGAGCTGT 345
QY 240 CACTGTCTGGGGTCTCTGGTAACTCTGCTGATGTGTGACTGTGAGGAGAGGA 299
Db 346 GATCATTTCTGGTCTCTGGAACCTGGCTTGATCATATATCTTGAACAAAGGA 405
QY 300 GAAAGCCAACTGACCACTGCTTATCGCAAGCTGGCTTCTGACTTCTTCACTTCTCATGTG 359
Db 406 GATGAGAAATGTTACCAACTCTTGAATGTAAGCTTCTTCTTCACTGCTTGTGTC 465
QY 360 CTTCTCTGCCAGCGGTGACCGCGCTTACACCATCATGCACTACTGGATCTTTGGAGA 419
Db 466 CATCATGTGTCTCCCTTTACATTTGTCTACACATTAATGACCACTGGGTCTTTGGTGA 525
QY 420 GACCTCTGCAAGATGTCGGCTTCACTCAGTGTGTCGGTACGTCTCCATCTCTC 479
Db 526 GCGGATGTGAAGTTGAATCTTTTGTGCAATGTTTCAATCACTGTGTCCATTTTCTC 585
QY 480 GCTGCTCTCTGGCCCTGGAGAGGCATCAGCTCATCATCAACCAACAGGCTGGAAGCC 539
Db 586 TCTGTTCTCATTTGTTGGAAAGACATCAGCTGATATCAACCTCGAGGGTGGAGACC 645
QY 540 CAGCATCTCAGGCTACCTGGGATGTCCTCATCTGGGTGATTTGGCTGTGTCCTCTC 599
Db 646 AAATAATAGACATGTTATGATAGTATGCTGTGATTTGGTCTGCTGTGGCTTCTTC 705
QY 600 CTTGCTCTCTGGCCCAACAGCATCTCTGGAATGTTCTTCCAAAGAACCACTCAAGGC 659
Db 706 TTTGCTTTCTGTATCTACCAAGTAATGACTGATG-----AGCGTTCCAAATGTAAC 759
QY 660 TCTGAGTTCTCTGGCAGATAGAGTGTCTGTACCGAGTCTCTGGGCACTGGCTACACCG 719
Db 760 ACTTGATGCTACAAAGACAAATACGTGTGTTTGTATCAATTTCCATCGGACTCTCATAG 819
QY 720 CACCATCTACACCACT 779
Db 820 GTTGTCTTATACCACT 879

QY 780 GGTCTGTTATGACGCATCTACCGCGCTGCGAGAGGCGGGCGCGTGTTCACAA----- 836
Db 880 TATTTGCTACTTCAAGATATATATACGCTTAAAGAGGAGAAACAACATGATGGACAAGAT 939
QY 837 GGGCACCTACAGCTTGCAGCTGGGCACATGAAGCAGGTCAATGTGGTGTCTGTGCTGTGAT 896
Db 940 GAGAGACAATAAGTACAGGTCCAGTGAACCAAAAGATCAATATCATGCTGTCTCCAT 999
QY 897 GGTGTGGCTTTGGCGTCTCTGCTGCTCTGCTGCTGATGTGTTCAACAGCCTGGAAGATG 956
Db 1000 TGTGTAGCATTTGCAGTCTGCTGCTCTCTCTTACCATCTTTTAAACACTGTGTTGATTG 1059
QY 957 GCACCATGAGGCCATCCCATCTGCGACGGGAACCTCATCTTCTTGTAGTGTGCCACTTGT 1016
Db 1060 GAATCATCATGATCATGTCTGCTGCAACCAACATCTGTATTTCTGCTCTGCCACTCAC 1119
QY 1017 TCCATGGCTCCACTCGCTCAACCCATTCACTATGCTTCTTCAACCAACCACTTCAA 1076
Db 1120 AGCAATGATATCCACTTGTGTCAACCCCATATTTTATGGTTCTCTGAAACAAAACCTTCCA 1179
QY 1077 GAAGGAGATCAAGGCCCTGGTCTGACTTCCGACAGAGCGCCCTCTGGAGGATCGGA 1136
Db 1180 GAGAGACTTGCAGTCTCTTCTTCACTTTTGTGATTTCCGCTCTCGGATGATGATATGA 1239
QY 1137 GCATCTGCCCTGTCCACAGTACATACGGAAGTCTTCAAAGGTCCTGAGGCTAAGTGG 1196
Db 1240 AACAAATAGCCATGTCCACGATGCACAGATGTTTCCAAAACCTTCTTTGAAGCAA-----G 1295
QY 1197 CAGTCCCAATCCCATTTAACAGGTCTA 1224
Db 1296 CAAGCCAGTCGCATTTAAAAAATCAA 1323

RESULT 11
US-10-410-648-3
; Sequence 3, Application US/10410648
; Publication No. US20040072847A1
; GENERAL INFORMATION:
; APPLICANT: Bakthavatchalam, Rajagopal
; APPLICANT: Blum, Charles A.
; APPLICANT: Brielmann, Harry L.
; APPLICANT: Dartow, James W.
; APPLICANT: De Lombaert, Stephane W.
; APPLICANT: Hutchinson, Alan W.
; APPLICANT: Tran, Jennifer W.
; APPLICANT: Elliott, Richard L.
; APPLICANT: Hammond, Marlys L.
; TITLE OF INVENTION: SPYRO[ISOBENZOFURAN-1,4'-PIPERIDIN]-3-ONES AND
; TITLE OF INVENTION: 3H-SPIRO[ISOBENZOFURAN-1,4'-PIPERIDINES
; FILE REFERENCE: U 014539-7
; CURRENT APPLICATION NUMBER: US/10/410,648
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: 10/013,846
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 60/254,990
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1605
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-410-648-3

Query Match 19.5%; Score 257.6; DB 12; Length 1605;
Best Local Similarity 55.0%; Pred. No. 2.5e-64;
Matches 576; Conservative 0; Mismatches 459; Indels 13; Gaps 3;

QY 180 TGAACATTCGCCAGGATTCGGTGGACGTGATGTTCTCATGTCACCTTCTTACAGCATTA 239
Db 286 TGAATGATGTCATCTGCCCTTGGCCATGATATTTACTTAGCTTGTCTATGAGCTGT 345

240 GACTGTCGTGGGGTCTCGGGTAACCTCTCGCTGATGTGTGACTGTGAGGAGGA 299
346 GATCATTTCTTGGTGTCTCTGAAACCTTGGCTTGTATCATATCTTGAACAAAGA 405
300 GAAAGCCAAAGTGAACCAACCTGCTTATCGCAACCTGGCTTCTGACTTCTCATGTG 359
406 GATGAGAAATGTTACCAACATCTCTGATTGTGAACCTTCTTCTCAGACTGTCTTGTGC 465
360 CCTCTCTGCGACCGGTGACCGGCTACACCATCATGACTACTGATCTTTGGAGA 419
466 CATCATGTGTCCTCCCTTACATTTGTCTACATTAATGACCATGAGTCTTTGGTGA 525
420 GACCTCTGCAAGATGTGGGCTTCACTCCAGTGTGCTGGTACGCTTCCATCTCTC 479
526 GGGCATGTGAAGTGAATCCTTTGTGCAATGTGTTCAATCACTGTGTCCATTTCTC 585
480 GCTGCTCTGTGGCCCTGAGAGGATCACTCATCATCAACCCACAGCTGGAGGC 539
586 TCTGGTTCTCATGCTGTGAACACATCACTGATTAATCAACCCCTGAGGGTGGAGCC 645
540 CAGCATCTCAGAGCCTACCTGGGGATTGTGCTCATCTGGGTCAATGCTCTCTCTC 599
646 AATAAATAGACATGCTTATGATGATTTGCTGTGATTTGGTCTTGTGCTGCTTCTC 705
600 CTTGCCCTTCTGCGCAACAGCATCTCTGGAGATGTCTTCCACAAACCACTCCAGGC 659
706 TTTGCCCTTCTGATCTACCAAGTAATGACTGATG-----AGCCGTTCAAAATGTAAC 759
660 TCTGGAGTCTCTGCGAGATGAAGTGTGCTGTACCGAGTCTCTGCGCACTGGCTCACCACCG 719
760 ACTGTATGCGGTACAAAGCAATACGTGTCTTTGATCAATTTCCATCGACTCTCATAG 819
720 CACCATCTACACACTTCTGCTCTCTTCCAGTACTGCTCTCCAGTCTGCGGCTTCTCT 779
820 GTTGTCTTATACCACTCTCTCTTGTGTGCTGCAATATTTTGGTCCATTTGTTTATAT 879
780 GGTCTGTTATGACGATCTACCGGCTGACAGGACGGGGCTGTTTCACAA--- 836
880 TATTTGCTACTTCAAGATATATATACGCTTAAAGAGAGAAACAATGATGACAGAT 939
837 GGGCACTACAGCTTGGAGCTGGGACATGAAGCAGGTCAATGTGGTGTCTGTGTGAT 896
940 GAGAGACAATGAATGACAGTCCAGTGAACCAAAAGAAATCAATATCATGCTCTCTCCAT 999
897 GGTGGTGGCTTTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 956
1000 TGTGTGATGATTTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1059
957 GCACCATGAGCCATCCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1016
1060 GAATCATCAGATCATTTGCTACCTGCAACCAACCAATCTGTTTCTGCTCTGCTGCTGCT 1119
1017 TGCCATGGCTTCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1076
1120 AGCAATGATATCCACTTGTGTGCAACCCCATATTTTATGGGTCTGTAACAAACACTTCA 1179
1077 GAAGGAGATCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1136
1180 GAGAGACTTGAGTCTTCTTCACTTTTGTGATTTTGGGTCTGCGGATGATGATATGA 1239
1137 GCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1196
1240 AACAATAGCCATGTCCAGATGTCACAGATGTTTCCAAAACCTTCTTTTGAAGCAA---G 1295
1197 CAGGTCCAATCCCATTTAAACAGGTCTA 1224
1296 CAAGCCAGTGGCATTTAAAAAATCAA 1323

RESULT 12

US-10-013-846-3

; Sequence 3, Application US/10013846

; Publication No. US20030036652A1

GENERAL INFORMATION:
; APPLICANT: Bakthavatchalam, Rajagopal
; APPLICANT: Blum, Charles A
; APPLICANT: Brielmann, Harry L
; APPLICANT: Darrow, James W
; APPLICANT: De Lombaert, Stephane
; APPLICANT: Hutchison, Alan
; APPLICANT: Tran, Jennifer
; APPLICANT: Zheng, Xiaozhang
; APPLICANT: Elliott, Richard L
; APPLICANT: Hammond, Marlys
; TITLE OF INVENTION: Spiro[isobenzofuran-1,4'-piperidin]-3-ones and
; FILE REFERENCE: 3H-spiroisobenzofuran-1,4'-piperidines
; CURRENT APPLICATION NUMBER: US/10/013,846
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: US 60/254,990
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1605
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-013-846-3

Query Match 19.5%; Score 257.6; DB 15; Length 1505;
Best Local Similarity 55.0%; Pred. No. 2.5e-64;
Matches 576; Conservative 0; Mismatches 459; Indels 13; Gaps 3;

QY 180 TGAACATTTGCCAGGATTCGGTGGAGCGTGAATGGTCTTATCGTCACTCTCTACAGATGA 239
Db 286 TGTGATTTGTATCTGCCCCCTTGGCCATGATATTTACCTTAGCTCTTGTATGAGCTGT 345
QY 240 GACTGTCGTGGGGTCTCTGGTAACTCTGCTGATGTGTGACTGTGAGGAGGAAGA 299
Db 346 GATCATTTCTTGGTGTCTCTGGAACCTGGCTTGTATCAATCATCTTGAACAAAGA 405
QY 300 GAAAGCCAAAGTGAACCAACCTGCTTATCGCAACCTGGCTTCTGACTTCTCATGTG 359
Db 406 GATGAGAAATGTTACCAACATCTCTGATTGTGAACCTTCTCTCAGACTGTGCTTCTC 465
QY 360 CTTCTCTGCGACCGCTGACCGGCTCTACACCATCATGACTACTGATCTTTGGAGA 419
Db 466 CATCATGTGCTCTCCCTTACATTTGTCTACATTAATGACCATGAGTCTTTGGTGA 525
QY 420 GACCTCTGCAAGATGTGGGCTTCACTCCAGTGTGCTGGTACGCTTCCATCTCTC 479
Db 526 GGGCATGTGAAGTGAATCCTTTGTGCAATGTGTTCAATCACTGTGTCTCTCTC 585
QY 480 GCTGCTCTGCTGGGCTTGGAGAGCATCAGTCTCATCATCAACCCACAGCTGGAAGCC 539
Db 586 TCTGGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 645
QY 540 CAGCATCTCAGAGCCTACCTGGGATTTGCTCATCTGGGTCAATGCTGCTGCTGCTGCT 599
Db 646 AATAAATAGACATGCTTATGATGATTTGCTGATTTGGGTCTGCTGCTGCTGCTGCTG 705
QY 600 CTTGCCCTTCTGCGCAACAGCATCTCTGGAGATGTCTTCCACAAACCACTCCAGGC 659
Db 706 TTTGCCCTTCTGATCTACCAAGTAATGACTGATG-----AGCCGTTCAAAATGTAAC 759
QY 660 TCTGGAGTCTCTGCGAGATGAAGTGTGCTGTACCGAGTCTCTGGGCACTGGCTCACCACCG 719
Db 760 ACTGTATGCGGTACAAAGCAATACGTGTCTTTGATCAATTTCCATCGACTCTCATAG 819
QY 720 CACCATCTACACACTTCTGCTCTCTTCCAGTACTGCTCTCCAGTCTGGGCTTCTCATCT 779
Db 820 GTTGTCTTATACCACTCTCTCTTGTGTGCTGCAATATTTTGGTCCATTTGTTTATAT 879
QY 780 GGTCTGTTATGACGATCTACCGGCTGACAGGACGGGGCTGTTTCACAA--- 836
Db 880 TATTTGCTACTTCAAGATATATATACGCTTAAAGAGAGAAACAATGATGAGCAAGAT 939

Db	706	TTTGCCTTTCTGATCTACCAAGTAATGACTGATG-----AGCGGTCCAAAATGTAAC	759
Qy	660	TCTGGAGTTTCTGCGACATAGAGTGGTCTGTACCGAGTCTCTGGCCACTGGCTCACCACCG	719
Db	760	ACTTGATGCGGTACAAAGACAAATACGTGTGCTTTGATCAATTTCCATCGGACTCTCATAG	819
Qy	720	CACCATCTACACCACTTCTGCTCTCTTCCAGTACTGCTCCCACTGGGCTTCATCCT	779
Db	820	GTTCCTTTATACCACTCTCTCTCTTGGTGTCTCAGTATTTTGGTCCACTTTGTTTATATT	879
Qy	780	GGTCTGTATGACAGCTCTATACCGCGGCTGTCAGAGCGAGGGGGCGGTGTTTCAAA---	836
Db	880	TATTTGCTACTTCAAGATATATATACGCCCTAAAGAGGAGAAACACATGATGGACACAGAT	939
Qy	837	GGGCACCTACAGCTTGGGAGCTGGGCACATGAGCAGGTCAATGTGTGTGTGGTGTGAT	896
Db	940	GAGAGACATAGTACAGGTCCAGTGAAACCAAGAAATCAATATCATGTGTCTCTCCAT	999
Qy	897	GGTGGTGGCTTTGCGGTGTCTCTGGTGGCTCTGCTGATGTGTTCAACAGCCTGGAGACTG	956
Db	1000	TGTGTAGCATTTGCAGTCTGTGGTCTCTTACCATCTTTAACACTGTGTGTGATTG	1059
Qy	957	GCACCATGAGGCCATCCCATCTGCCAGGGAACCTCATCTTCTAGTGTGCCACTTGTCT	1016
Db	1060	GAATCATCAGATCATTTGTCTGCAACCAACATCTGTATTTCTGTCTGTGCCACTCAC	1119
Qy	1017	TGCCATGGCTCCACCTGCTCAACCCATTCATCTATGGCTTTCTCAACACCACTTCAA	1076
Db	1120	AGCAATGATATCCACTTGTGTCAACCCCATATTTTATGGGTCTCTGAACAAAACTTCCA	1179
Qy	1077	GAAGAGATCAAGGCCCTGGTGTGCTGACTTGCAGCAGAGCGCCCCCTGGAGGAGTCGA	1136
Db	1180	GAGAGACTTGCAGTCTCTTCAACTTTTGTGATTTCCGGTCTCGGATGATGATTATGA	1239
Qy	1137	GCATCTGCCCTGTCCACAGTACATACGAAAGTCTCCAAAGGGTCCCTGAGGCTTAAGTG	1196
Db	1240	AACATAGCCATGTCCACGATGCCACAGATGTTTCCAAAACCTTCTTTGAAGCAA----	1295
Qy	1197	CAGTCCAAATCCCATTTAACAGGTCTA	1224
Db	1296	CAAGCCAGTCGCATTTAAAAAATCAA	1323

Search completed: May 11, 2004, 11:01:35
Job time : 588 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2004, 12:50:36 ; Search time 58 Seconds
(without alignments)
1826.816 Million cell updates/sec

Title: US-09-430-775-2

Perfect score: 1965
Sequence: 1 MNTSHLLALLPRSPQGNR.....TVHTEVSKGSLRSLGRSNPI 375

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001s.*
- 5: Geneseq2002s.*
- 6: Geneseq2003as.*
- 7: Geneseq2003bs.*
- 8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1965	100.0	375	4	AAE06691 Human neu
2	1965	100.0	375	5	ABP81946 Human neu
3	1965	100.0	375	6	ABP81946 Human neu
4	1956	99.5	375	6	ABP81946 Human neu
5	1519	77.3	375	6	ABG73518 Murine NY
6	1494	76.0	375	6	ABG73518 Murine NY
7	1494	76.0	375	6	ABG73517 Rat NY4R
8	960	48.9	375	6	ABG73520 D. rerio
9	869	44.2	382	4	AAE08001 Rat neuro
10	867.5	44.1	382	4	ABG73519 C. porcel
11	867	44.1	382	2	AAW02101 Mouse neu
12	863	43.9	371	2	AAW02099 Mouse neu
13	860.5	43.8	384	5	ABP81946 Human neu
14	856.5	43.6	383	3	AAE08000 Human neu
15	856.5	43.6	384	2	AAE08000 Human neu
16	856.5	43.6	384	2	AAE08000 Human neu
17	856.5	43.6	384	4	AAE08000 Human neu
18	856.5	43.6	384	4	AAE08000 Human neu
19	856.5	43.6	384	4	AAE08000 Human neu
20	856.5	43.6	384	4	AAE08000 Human neu
21	856.5	43.6	384	4	AAE08000 Human neu
22	856.5	43.6	384	5	AAU10585 Human neu
23	856.5	43.6	384	5	AAU10585 Human neu
24	856.5	43.6	384	6	ABJ37037 Human bre
25	856.5	43.6	384	6	ABR47546 Breast ca

26	856.5	43.6	384	6	ABP81946 Human neu
27	856.5	43.6	384	6	AAO23265 Human neu
28	856.5	43.6	384	7	ABW01461 Human neu
29	855	43.5	398	2	AAW03014 Modified
30	854.5	43.5	411	2	AAW03012 Neurosept
31	847	43.1	371	6	ABG73518 Rabbit NY
32	846.5	43.1	388	4	AAE06688 Human neu
33	841	42.8	383	2	AAE06688 Human neu
34	830.5	42.3	399	2	AAE06688 Human neu
35	823.5	41.9	370	2	AAW02100 Human neu
36	710.5	36.2	307	2	AAE07196 Mouse neu
37	705.5	35.9	301	2	AAE08751 G-protein
38	705.5	35.9	301	2	AAE08751 G-protein
39	573	29.2	290	6	AAE06693 Human neu
40	573	29.2	290	6	ABP81946 Human neu
41	561.5	28.6	383	4	AAE08015 Pig chime
42	560.5	28.5	383	4	AAE08009 Dog chime
43	557	28.3	395	4	AAE08013 Rat chime
44	556.5	28.3	394	4	AAE08005 Human ch
45	556.5	28.3	394	5	ABB79512 Chimeric

ALIGNMENTS

RESULT 1
AAE06691
ID AAE06691 standard; protein; 375 AA.
XX AAE06691;
AC AAE06691;
XX 16-OCT-2001 (first entry)
DT Human neuroptide Y (NPY) Y4 receptor.
DE Human neuroptide Y (NPY) Y4 receptor.
XX Human neuroptide Y; NPY; bone disease; bone mass; gene therapy;
KW cerebrospinal fluid; CSF; inositol phosphate; IP; Paget's disease;
KW fracture; extracellular signal-regulated kinase; ERK; osteoporosis;
KW osteopenia; bone metastasis; neurotransmitter; osteogenic;
KW NPY Y4 receptor.
XX Homo sapiens.
XX WO200153477-A1.
XX 26-JUL-2001.
XX 22-JAN-2001; 2001WO-US002040.
XX 20-JAN-2000; 2000US-00489872.
XX (BAYU) BAYLOR COLLEGE MEDICINE.
XX (AWLI/) AWLING M.
XX Amling M, Karsenty G, Ducey P;
XX WPI; 2001-488709/53.
XX N-PSDB; AAD12802.
XX Treating or preventing reduced bone mass, e.g. osteoporosis, by reducing
XX the level of neuroptide Y activity in blood or cerebrospinal fluid.
XX Example 7; Page 86; 102pp; English.

The present invention relates to a method for treatment or prevention of bone diseases characterised by loss of bone mass, comprises administering to a mammal a compound that lowers the level of neuroptide Y (NPY) in the serum or cerebrospinal fluid (CSF) or a compound that lowers the level of inositol phosphate (IP) or extracellular signal-regulated kinase (ERK). The method is specifically used to treat (including by gene therapy) or prevent osteoporosis, osteopenia or Paget's disease, but may also be used e.g., in cases of fractures or bone metastases. These diseases may also be diagnosed by detecting elevated NPY levels.

QY 301 NLIFLVCHLLAMASTCVNPFYIGFLNTNFKKEIKALVLTCCQSAPLESEHPLSTVHTE 360
DB 301 NLIFLVCHLLAMASTCVNPFYIGFLNTNFKKEIKALVLTCCQSAPLESEHPLSTVHTE 360
QY 361 VSKGSLRLSGRSNPI 375
DB 361 VSKGSLRLSGRSNPI 375

RESULT 3

ABP81859
ID ABP81859 standard; protein; 375 AA.

AC
XX
XX
DT 04-MAR-2003 (first entry)
XX
DE Human neuropeptide Y receptor type 4 protein SEQ ID NO:203.

KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer.

XX Homo sapiens.

OS WO200261087-A2.

PN 08-AUG-2002.

PD 19-DEC-2001; 2001WO-US050107.

PF 19-DEC-2000; 2000US-0257144P.

PR (LIFE-) LIFESPAN BIOSCIENCES INC.

PA Burmer GC, Roush CL, Brown JP;

PI WPI; 2003-046718/04.

XX N-PSDB; ABZ42706.

XX New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT autoimmune diseases.

PS Disclosure; Fig 1; 523pp; English.

XX The present invention describes antigenic peptides (I) comprising: (a)
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related diseases, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,

CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnoses. ABZ42523 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention

XX Sequence 375 AA;

QY Query Match 100.0%; Score 1965; DB 6; Length 375;

DB Best Local Similarity 100.0%; Pred. No. 7.3e-193; Indels 0; Gaps 0;
Matches 375; Conservative 0; Mismatches 0;

QY 1 MNTSHLLALLPKSPQGENRSKPLGTPYNFSEHCQDSVDMVFIVTSYSIETVVGVLGNL 60

DB 1 MNTSHLLALLPKSPQGENRSKPLGTPYNFSEHCQDSVDMVFIVTSYSIETVVGVLGNL 60

QY 61 CLMCVTVRQKEKANTNLLIANLAFSDFLMCLLCOPLTAVTINDYWFGETLCKMSAPI 120

DB 61 CLMCVTVRQKEKANTNLLIANLAFSDFLMCLLCOPLTAVTINDYWFGETLCKMSAPI 120

QY 121 QCMSTVTSILSLVALERHQLIINPTGKPSISQAYLGIVLWIAVCVLSLPLANSIL 180

DB 121 QCMSTVTSILSLVALERHQLIINPTGKPSISQAYLGIVLWIAVCVLSLPLANSIL 180

QY 181 ENVFHNKHSKALEFLADKVVCTESWPLAHRITTYTFLLLFOYCLPLFCVLYRIYR 240

DB 181 ENVFHNKHSKALEFLADKVVCTESWPLAHRITTYTFLLLFOYCLPLFCVLYRIYR 240

QY 241 LORQGRVFKHGYSIRAGHKMKNVVLVVMVAVLWPLHVFNSLEDWHHEAIPICHG 300

DB 241 LORQGRVFKHGYSIRAGHKMKNVVLVVMVAVLWPLHVFNSLEDWHHEAIPICHG 300

QY 301 NLIFLVCHLLAMASTCVNPFYIGFLNTNFKKEIKALVLTCCQSAPLESEHPLSTVHTE 360

DB 301 NLIFLVCHLLAMASTCVNPFYIGFLNTNFKKEIKALVLTCCQSAPLESEHPLSTVHTE 360

QY 361 VSKGSLRLSGRSNPI 375

DB 361 VSKGSLRLSGRSNPI 375

RESULT 4

AAR79119

ID AAR79119 standard; protein; 375 AA.

XX AAR79119;

XX 07-DEC-1995 (first entry)

DT Neuropeptide Y/peptide YV/pancreatic polypeptide receptor (Y4).

DE Y4 receptor; hp25a neuropeptide receptor; antisense oligonucleotide;
KW therapeutic.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Region 39..66 /note= "transmembrane spanning region I"

FT Region 78..104 /note= "transmembrane spanning region II"

FT Region 118..137 /note= "transmembrane spanning region III"

FT Region 156..178 /note= "transmembrane spanning region IV"

FT Region 212..235 /note= "transmembrane spanning region V"

FT Region 263..288 /note= "transmembrane spanning region VI"

FT Region 302..326 /note= "transmembrane spanning region VII"

XX WO9517906-A1.
 XX 06-JUL-1995.
 XX 28-DEC-1994; 94WO-US014436.
 XX 28-DEC-1993; 93US-00176412.
 XX (SYNA-) SYNAPTIC PHARM CORP.
 XX Bard JA, Walker MW, Brancheck T, Weinshank RL;
 XX WPI; 1995-246190/32.
 XX N-PSDB; AAQ94171.
 XX New nucleic acid encoding a Y4-Receptor, anti-sense mols. and ligands -
 XX useful for treating amnesia, feeding/sleeping disorders or epilepsy, etc.
 XX Disclosure; Fig 1; 154pp; English.
 XX The sequence represents a human neuropeptide Y/peptide YY/ pncretic
 XX polypeptide (Y4) receptor, which can be used to screen drugs which bind
 XX to it, specifically to find ligands (agonists or antagonists) which bind
 XX to it. The ligands can be used to treat abnormalities, specifically the
 XX antagonists can be used to treat amnesia, feeding disorders, epilepsy,
 XX hypertension, sleeping disorders or pain
 XX Sequence 375 AA;
 SQ Query Match 99.5%; Score 1956; DB 2; Length 375;
 Best Local Similarity 99.5%; Pred. No. 6.1e-192;
 Matches 373; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MNTSHLLALLPKSPQGENRSKPLGTPYNFSEHCQDSVDMVFIVTSYIETVGVGLNL 60
 Db 1 MNTSHLLALLPKSPQGENRSKPLGTPYNFSEHCQDSVDMVFIVTSYIETVGVGLNL 60
 QY 61 CLMCVTVROKESKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGTCRMSAFI 120
 Db 61 CLMCVTVROKESKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGTCRMSAFI 120
 QY 121 QCMSTVTSILSLVALERHQLINPTGWKPSISQAYLGIWLVIAVLSLPLANSIL 180
 Db 121 QCMSTVTSILSLVALERHQLINPTGWKPSISQAYLGIWLVIAVLSLPLANSIL 180
 QY 181 ENVFHKNHSALEFLADKVVCCTESWPLAHHRTIYTTFLLLFYQCLPLGILVCYARIYR 240
 Db 181 ENVFHKNHSALEFLADKVVCCTESWPLAHHRTIYTTFLLLFYQCLPLGILVCYARIYR 240
 QY 241 LORQGRVPHKGTYSLRAGHKQNVNVLVWVAVAVLWPLHVFNSLEDWHHEAIPICHG 300
 Db 241 LORQGRVPHKGTYSLRAGHKQNVNVLVWVAVAVLWPLHVFNSLEDWHHEAIPICHG 300
 QY 301 NLIFLVCHLLAMASTCVPNTFYGLNTNFKEIKALVLTCCQSAPLESEHPLSTVHTE 360
 Db 301 NLIFLVCHLLAMASTCVPNTFYGLNTNFKEIKALVLTCCQSAPLESEHPLSTVHTE 360
 QY 361 VSKGSLRLSGRSNPI 375
 Db 361 VSKGSLRLSGRSNPI 375
 RESULT 5
 ABG73516
 ID ABG73516 standard; protein; 375 AA.
 XX
 AC ABG73516;
 XX
 XX 14-FEB-2003 (first entry)
 DT
 XX Murine NY4R protein SEQ ID 47.
 DE
 XX

KW G-protein coupled receptor; HGPBMY1; HGPBMY2; immunosuppressive;
 KW cardiant; neuroprotective; antiinflammatory; cytostatic; vulnerary;
 KW vaccine; gene therapy; autoimmune; cardiovascular; neural; reproductive;
 KW haematopoietic; pulmonary; gastrointestinal; proliferation; cell cycle;
 KW birth defect; aberrant phosphorylation; acute phase response; receptor;
 KW signal transduction; hyperimmune activity; inflammatory; hypercongenital;
 KW necrotic lesion; wound; organ transplant rejection.
 XX Mus musculus.
 OB
 FN WO200268591-A2.
 XX
 XX 06-SEP-2002.
 PD
 XX 22-FEB-2002; 2002WO-US005281.
 PF
 XX 23-FEB-2001; 2001US-0270792P.
 PR 23-FEB-2001; 2001US-0270793P.
 PR 06-JUN-2001; 2001US-0296427P.
 XX
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 PA
 XX Feder J, Ramanathan C, Nelson T, Mintier G, Cacace A, Barber L;
 PI Kornacker M, Bol D;
 XX WPI; 2003-058304/05.
 DR
 XX New human HGPBMY1 or HGPBMY2 polynucleotide and polypeptide, useful
 PT preventing, treating or ameliorating a disorder e.g., wound,
 PT cardiovascular disorder or transplant rejection.
 XX
 XX Disclosure; Fig 9; 316pp; English.
 PS
 XX This invention describes the novel human G-protein coupled receptors
 CC (GPCR's), HGPBMY1 or HGPBMY2 which have immunosuppressive, cardiant,
 CC neuroprotective, antiinflammatory, cytostatic and vulnerary activity and
 CC can be used in vaccines or for gene therapy. Pharmaceutical compositions
 CC comprising HGPBMY1 or HGPBMY2 polypeptides or their agonists or
 CC antagonists or modulators, or a HGPBMY1- or HGPBMY2-specific antibody
 CC are useful for preventing, treating or ameliorating a medical condition
 CC comprising autoimmune, cardiovascular, neural, reproductive,
 CC haematopoietic, pulmonary, gastrointestinal or proliferating disorder, a
 CC cell cycle or birth defect, a disorder related to aberrant
 CC phosphorylation, acute phase responses or signal transduction or to
 CC hyperimmune activity, an inflammatory or hypercongenital condition, a
 CC necrotic lesion, a wound, organ transplant rejection or a condition
 CC related to organ transplant rejection. This sequence represents a G-
 CC protein coupled receptor associated with the human HGPBMY proteins
 CC described in the disclosure of the invention
 XX
 SQ Sequence 375 AA;

Query Match 77.3%; Score 1519; DB 6; Length 375;
 Best Local Similarity 75.9%; Pred. No. 4.5e-147;
 Matches 283; Conservative 35; Mismatches 55; Indels 0; Gaps 0;
 QY 1 MNTSHLLALLPKSPQGENRSKPLGTPYNFSEHCQDSVDMVFIVTSYIETVGVGLNL 60
 Db 1 MNTSHFLAPLPGSLQKNGTNPLDSPYNFSDGQDSAEALLAFITTSIETILGVGLNL 60
 QY 61 CLMCVTVROKESKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGTCRMSAFI 120
 Db 61 CLIFVTTRQEKSNVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGTCRMSAFI 120
 QY 121 QCMSTVTSILSLVALERHQLINPTGWKPSISQAYLGIWLVIAVLSLPLANSIL 180
 Db 121 QCMSTVTSILSLVALERHQLINPTGWKPSISQAYLGIWLVIAVLSLPLANSIL 180
 QY 181 ENVFHKNHSALEFLADKVVCCTESWPLAHHRTIYTTFLLLFYQCLPLGILVCYARIYR 240
 Db 181 NDLFHYNHSKVVEFLEDKVVCFSWSSDHRLLIYTTFLLLFYQCIPLAFILVCYIRIYR 240
 QY 241 LORQGRVPHKGTYSLRAGHKQNVNVLVWVAVAVLWPLHVFNSLEDWHHEAIPICHG 300

Db	241	LQROKHVFHAHACSSRAGOMKRINSMLMTWMTAPAVLWLPFHVFTLEDWYQEAIPACHG	300
Qy	301	NLIFLVCHLLAVASTCVNPFFYIGPLNTWFKKEIKALVLTQQAPLEESRHLPSTVHT	360
Db	301	NLIFLVCHLLAVASTCVNPFFYIGPLNTWFKKEIKALVLTQQAPLEESRHLPSTVHT	360
Qy	361	VSKGSLRLSGRNS 373	
Db	361	LSKGSNRMGSKNS 373	
RESULT 6			
AAR79120			
ID AAR79120 standard; protein; 375 AA.			
XX	AC		
XX	AC		
XX	DT	AAR79120;	
XX	DT	09-DEC-1995 (first entry)	
XX	DE	Neuropeptide Y/peptide Y/pancreatic polypeptide receptor (Y4).	
XX	DE		
XX	KW	Y4 receptor; hp25a neuropeptide receptor; antisense oligonucleotide;	
KW	KW	therapeutic.	
XX	XX		
OS	Rattus rattus.		
XX	XX		
FH	Key	Location/Qualifiers	
FT	Region	39..66	
FT	Region	/note= "transmembrane spanning region I"	
FT	Region	78..104	
FT	Region	/note= "transmembrane spanning region II"	
FT	Region	118..137	
FT	Region	/note= "transmembrane spanning region III"	
FT	Region	156..178	
FT	Region	/note= "transmembrane spanning region IV"	
FT	Region	212..235	
FT	Region	/note= "transmembrane spanning region V"	
FT	Region	263..288	
FT	Region	/note= "transmembrane spanning region VI"	
FT	Region	302..326	
FT	Region	/note= "transmembrane spanning region VII"	
XX	XX		
PN	WO9517906-A1.		
XX	XX		
XX	XX		
PD	06-JUL-1995.		
XX	XX		
PF	28-DEC-1994; 94WO-US014436.		
XX	XX		
PR	28-DEC-1993; 93US-00176412.		
XX	XX		
PA	(SYNA-) SYNAPTIC PHARM CORP.		
XX	XX		
PI	Bard JA, Walker MW, Branchek T, Weinshank RL;		
XX	XX		
DR	WPI; 1995-246190/32.		
DR	N-PSDB; AAQ94172.		
XX	XX		
PT	New nucleic acid encoding a Y4-Receptor, anti-sense mols. and ligands -		
PT	useful for treating amnesia, feeding/sleeping disorders or epilepsy, etc		
XX	XX		
PS	Disclosure; Fig 3; 154pp; English.		
XX	XX		
CC	The sequence represents a rat neuropeptide Y/peptide YY/ pancreatic		
CC	polypeptide (Y4) receptor, which can be used to screen drugs which bind		
CC	to it, specifically to find ligands (agonists or antagonists) which bind		
CC	to it. The ligands can be used to treat abnormalities, specifically the		
CC	antagonists can be used to treat amnesia, feeding disorders, epilepsy,		
CC	hypertension, sleeping disorders or pain		
XX	XX		
SQ	Sequence 375 AA;		

Best Local Similarity 75.1%; Pred.No. 1.7e-144;
Matches 280; Conservative 35; Mismatches 58; Indels 0; Gaps 0

QY 1 MNTSHLLALLPKSPQGENRSPKLPFPYFNFSHEHODSDVMVFIVTSYSIETVGVGLNL 60
Ddb 1 MNTSHLMASLSPAFLQCKNGTNPFLSDSLYNLSDGQDSADLLAFITTYSVETLVGLNL 60
QY 61 CLMCVTVROKEKANVTNLLIANLAFSDFLMCLLCOPLTAVVTIMDYWIFGETLCKMSAFI 120
Ddb 61 CLIFVTRQKEKSNVTNLLIANLAFSDFLMCLLCOPLTAVVTIMDYWIFGELCKMLTFI 120
QY 121 QCMSVTVSIISLVVALERHQLIINPTGWNKPSISQAYLGIVLIWVIACVLSLPFLANSIL 180
Ddb 121 QCMSVTVSIISLVVALERHQLIINPTGWNKPSISQAYLGIVLIWVIFISCFSLSPFLANSIL 180
QY 181 ENWFHKHSKALBFLADKVVCTESPLAHRRIYTFELLFQYCLPLGFIILVCVARIYR 240
Ddb 181 NDLFPHYHNSKVFELEDKVVCFVSNSSDHRRIYTFELLFQYCLPLGFIILVCVARIYR 240
QY 241 LQROGRVFHKGTYSLRAGHKQNVNVLVWVAFVLMPLFLHFNLSLEDWHHEAIPICHG 300
Ddb 241 LQQRERAFHTHCSSRVGQMRINGMLMAMVTAFAVLMLFLHVFLELDWYQEAIPACHG 300
QY 301 NLIFLVCHLLAMASTCVNPIYGFILNTNFKKEIKALVLTQQSAPLESEHPLSTVHTE 360
Ddb 301 NLIFLVCHLLAMASTCVNPIYGFILNTNFKKEIKALVLTQQSAPLESEHPLSTVHTE 360
QY 361 VSKGSLRLSGESN 373
Ddb 361 LSKGSMRMGSKSN 373

RESULT 7
ABG73517
ID ABG73517 standard; protein, 375 AA.
XX ABG73517;
AC XX
DT 14-FEB-2003 (first entry)
XX
XX
DE Rat NY4R protein SEQ ID 48.
XX
XX G-protein coupled receptor; HGPBWMY1; HGPBWMY2; immunosuppressive;
KW cardian; neuroprotective; antiinflammatory; cytostatic; vulnerary;
KW vaccine; gene therapy; autoimmune; cardiovascular; neutral; reproductive;
KW haematopoietic; pulmonary; gastrointestinal; proliferation; cell cycle;
KW birth defect; aberrant phosphorylation; acute phase response; receptor;
KW signal transduction; hyperimmune activity; inflammatory; hypercongenital;
KW necrotic lesion; wound; organ transplant rejection.
XX
OS Rattus sp.
XX
XX WO200268591-A2.
XX
XX
PD 06-SEP-2002.
XX
XX 22-FEB-2002; 2002WO-US005281.
PF
XX 23-FEB-2001; 2001US-0270792P.
XX 23-FEB-2001; 2001US-0270792P.
PR 06-JUN-2001; 2001US-0296427P.
XX
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
PA
XX Feder J, Ramanathan C, Nelson T, Mintier G, Cacace A, Barber L;
PI Kornacker M, Bol D;
XX
XX WPI; 2003-058304/05.
XX
XX New human HGPBWMY1 or HGPBWMY2 polynucleotide and polypeptide, useful
PT preventing, treating or ameliorating a disorder e.g., wound,
PT cardiovascular disorder or transplant rejection.
XX

Query Match

76.0%; Score 1494; DB 2; Length 375;

Disclosure; Fig 3; 154pp; English.

The sequence represents a rat neuropeptide Y/peptide YY/ pancreatic polypeptide (YY) receptor, which can be used to screen drugs which bind to it, specifically to find ligands (agonists or antagonists) which bind to it. The ligands can be used to treat abnormalities, specifically the antagonists can be used to treat amnesia, feeding disorders, epilepsy, hypertension, sleeping disorders or pain.

XX
XX
XX Feder J, Ramanathan C, Nelson T, Mintier G, Cacace A, Barber L;
PI Kornacker M, Bol D;
XX
XX WFI; 2003-058304/05.
DR
XX New human HGPBMV1 or HGPBMV2 polynucleotide and polypeptide, useful
PT preventing, treating or ameliorating a disorder e.g., wound,
PT cardiovascular disorder or transplant rejection.

Db 345 TGITKGSILNSGS 359

RESULT 9
AAE08001
ID AAE08001 standard; protein; 382 AA.
XX
AC AAE08001;
XX
DT 01-NOV-2001 (first entry)
XX
DE Rat neurotrophin Y1 (NPY1) receptor.
XX
KW Neurotrophin Y; NPY receptor; G-protein-coupled transmembrane protein;
KW transmembrane; TM domain; therapy; obesity; blood pressure; epilepsy;
KW Huntington's disorder; Parkinson's disorder; eating disorder; seizure;
KW locomotor; anxiety disorder; limbic seizure; tranquilliser; rat.
XX
OS Rattus norvegicus.
XX
FH Key Location/Qualifiers
FT Domain 231..262
FT /note= "Third intracellular loop domain"
XX
PN WO200155103-A2.
XX
PD 02-AUG-2001.
XX
PF 29-JAN-2001; 2001WO-US002804.
XX
PR 28-JAN-2000; 2000US-0178652P.
XX
PA (NEUR-) NEUROGEN CORP.
XX
PI Bennett M, Brodbeck R, Krause J;
XX
DR WPI; 2001-514543/56.
XX
PT New chimeric receptor proteins comprising a single polypeptide chain of
PT amino acids, useful as targets for drug actions, and as basis for drug
PT discovery and development.
XX
PS Disclosure; Page 46-47; 72pp; English.
XX
CC The present invention relates to chimeric neurotrophin Y (NPY) receptors.
CC The NPY receptors are G-protein-coupled transmembrane proteins with seven
CC membrane spanning transmembrane (TM) domains. The compounds that modulate
CC the activity of a NPY receptor is useful in the preparation of a
CC medicament for treating conditions including obesity, high/low blood
CC pressure, epilepsy, Huntington's and Parkinson's disorder and eating,
CC seizure, locomotor and anxiety disorders. They can also be used as
CC targets for drug actions, and as basis for drug discovery and
CC development. The NPYs receptor may have an anti-epileptic activity in the
CC control of limbic seizures. The present sequence is rat NPY1 receptor
XX
SQ Sequence 382 AA;
Query Match 44.2%; Score 869; DB 4; Length 382;
Best Local Similarity 46.8%; Pred. No. 2.5e-80;
Matches 168; Conservative 74; Mismatches 101; Indels 16; Gaps 4;
QY 28 YNFSEH-----CQSDVDVWVFIYTSYISFTVGVGLNCLMCVTVRQKEKAVNTN 77
DB 16 YNVSENSPFLAPENDCHPLAVIFTLALAYGAVILGVSGNALIIILKQKERNVTN 75
QY 78 LIANLASDFLMCLLCPLTAVYTIMDYIFGETLCKMSAFICOMSVTVSILSLVAL 137
DB 76 ILIIVNLSFDLVAVMCFPTFTYIMDRHWVGETMCKNLFVQCVSITVIFSLVLAV 135
QY 138 ERHQIINPTGKPSIOAYLGVILWIVACVLSLPLFLANGILENVFHNHKSKELEFLAD 197
DB 136 ERHQIINPTGKPSIOAYLGVILWIVACVLSLPLFLANGILENVFHNHKSKELEFLAD 193

QY 198 KVVCTESWPLAHHRTIYTTLLFOYCLPLGLFVLCYARIYRRLQROGRVPHKGTYS-LR 256
DB 194 KVCDFKPSDSHRLSYTTLLVLQYFGPLCFIFCYFKIYIRLKRNMMDKIDSKYR 253
QY 257 AGHKQVNVVVLVWVAFVAVLWLPJHVFNSLEBWHHEAIPICHGNLIFVCHLLAMASTC 316
DB 254 SSETKRINVMLLSIVVAFVAVCWLPITFTNTVDMNHQIATCNHLLFLCHLTAMISTC 313
QY 317 VNPFIYGLNTNFKEIKALVLTCCQSAPLESEHLPSTVHTVEYSGKSLRSGRSNPI 375
DB 314 VNPFIYGLNTNFKEIKALVLTCCQSAPLESEHLPSTVHTVEYSGKSLRSGRSNPI 369

RESULT 10
ABG73519
ID ABG73519 standard; protein; 383 AA.
XX
AC ABG73519;
XX
DT 14-FEB-2003 (first entry)
XX
DE C. porcellus G-protein coupled receptor SEQ ID 50.
XX
KW G-protein coupled receptor; HGPBMY1; HGPBMY2; immunosuppressive;
KW cardiac; neuroprotective; antiinflammatory; cytostatic; vulnerary;
KW vaccine; gene therapy; autoimmune; cardiovascular; neural; reproductive;
KW haematopoietic; pulmonary; gastrointestinal; proliferation; cell cycle;
KW birth defect; aberrant phosphorylation; acute phase response; receptor;
KW signal transduction; hyperimmune activity; inflammatory; hypercongenital;
KW necrotic lesion; wound; organ transplant rejection.
XX
OS Cavea porcellus.
XX
PN WO200268591-A2.
XX
PD 06-SEP-2002.
XX
PF 22-FEB-2002; 2002WO-US005281.
XX
PR 23-FEB-2001; 2001US-0270792P.
XX
PR 23-FEB-2001; 2001US-0270793P.
XX
PR 06-JUN-2001; 2001US-0296427P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Feder J, Ramanathan C, Nelson T, Mantiar G, Cacace A, Barber L;
PI Kornacker M, Bol D;
XX
DR WPI; 2003-058304/05.
XX
PT New human HGPBMY1 or HGPBMY2 polynucleotide and polypeptide, useful
PT preventing, treating or ameliorating a disorder e.g., wound,
PT cardiovascular disorder or transplant rejection.
XX
PS Disclosure; Fig 9; 316pp; English.
XX
CC This invention describes the novel human G-protein coupled receptors
CC (GPCR's), HGPBMY1 or HGPBMY2 which have immunosuppressive, cardiac,
CC neuroprotective, antiinflammatory, cytostatic and vulnerary activity and
CC can be used in vaccines or for gene therapy. Pharmaceutical compositions
CC comprising HGPBMY1 or HGPBMY2 polypeptides or their agonists or
CC antagonists or modulators, or a HGPBMY1- or HGPBMY2-specific antibody
CC are useful for preventing, treating or ameliorating a medical condition
CC comprising autoimmune, cardiovascular, neural, reproductive,
CC haematopoietic, pulmonary, gastrointestinal or proliferating disorder, a
CC cell cycle or birth defect, a disorder related to aberrant
CC phosphorylation, acute phase responses or signal transduction or to
CC hyperimmune activity, an inflammatory or hypercongenital condition, a
CC necrotic lesion, a wound, organ transplant rejection or a condition
CC related to organ transplant rejection. This sequence represents a G-
CC protein coupled receptor associated with the human HGPBMY proteins
CC described in the disclosure of the invention
XX


```
XX PS Claim 38; Page 49-50; 65pp; English.
XX CC Mouse neuropeptide Y Yx (NPY Yx) receptor (AAW02039), a novel subtype of
XX CC NPY, is a G-protein coupled receptor having 7 transmembrane-spanning
XX CC domains. Its amino acid sequence was deduced from a genomic DNA fragment
XX CC (AAT3127) obtd. from a mouse cosmid library. Vectors were constructed to
XX CC allow expression of the murine NPY Yx receptor in mammalian (COS-7)
XX CC cells. The recombinant receptor, or transformed host cells, can be used
XX CC to screen for cpds. that modulate the function of the receptor, or
XX CC modulate the expression of nucleic acids encoding the receptor. Such
XX CC cpds. are useful for treating a variety of disease conditions
XX PS Sequence 371 AA;
XX PS Query Match 43.9%; Score 863; DB 2; Length 371;
XX PS Best Local Similarity 43.2%; Pred. No. 9.9e-80;
XX PS Matches 156; Conservative 89; Mismatches 108; Indels 8; Gaps 5;
QY 12 PKSPGQENRKRPLGTPYNFSEHCQSDVDVMVFIVTSYSIETVVGVLNCLMCVTV-RQK 70
Db 10 PNKTSGRKNN-----SAPFYFSCQPPFLAILLLLIATVILINGIFGNLSIIIIIPKKR 65
QY 71 EKAVNTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFIQCMSVTVSIL 130
Db 66 EAQNVNTNILLIANLSLSDILVCMCIPTFTVIYTLMDHWVFGNTMCKLASYVQSVSVSIF 125
QY 131 SLVLVALERHOLIINPTGKPKESISOAYLIGVLIWIAVCLSLP-FLANSILENVFHKNS 189
Db 126 SLVLAIERYQLIINVRGKPRVAHAYWGLIIILISLTSIPFLSYHLTNEPFL-NLS 184
QY 190 KALFLADKVVCTESWPLAHRTIYTFLLFQYCLPLGFLVVCYARIYRLQSGR-VF 248
Db 185 LPTDIYTHQVACVEIWPSPKQLLFSTSLFMQLYFVPLGFLIICYLKIVLCRLKRRTRQVD 244
QY 249 HKGTYSLRAGHKQNVVLYVMVAVLVLPLHVSLEMDHEATPICHGNLIPLVCH 308
Db 245 RKXENKSLNENKRVNMLISIVTFGACWPLFIWFIWYHEMLMSCHDLVFFVCH 304
QY 309 LIAMASTCWNPFYIGFLNTNFKKIKALVLTQQSAPLESEHPLSTVHTVEVSKSLRL 368
Db 305 LIAMVSTCINPLFYGLNKNFKQDLMLLIHHCWCGEPQESYENIAMSTMTDESKSLKL 364
QY 369 S 369
Db 365 A 365
RESULT 13
ABB84499
ID ABB84499 standard; protein; 384 AA.
AC ABB84499;
XX 20-DEC-2002 (first entry)
XX Human hippocampus Y1 receptor protein.
DE Human; hippocampus; Y5; receptor; feeding behaviour; Y5 receptor;
XX food consumption; metabolic; anorectic; antidepressant; tranquiliser;
XX antiemetic; analgesic; hypotensive; cerebroprotective; cardiant;
XX antidiarhoeic; haemostatic; vaccine; anorexia; obesity; bulimia;
XX sexual disorder; reproductive disorder; depression; anxiety; memory loss;
XX migraine; pain; epileptic seizure; hypertension; cerebral haemorrhage;
XX shock; congestive heart failure; sleeve disturbance; nasal congestion;
XX diarrhoea; Y1.
XX OS Homo sapiens.
XX Key Location/Qualifiers
XX Domain 40..66 /label= transmembrane_domain_1
XX FT 77..99
XX Domain
```

```
FT Domain
FT 115..136 /label= transmembrane_domain_II
FT 155..177 /label= transmembrane_domain_III
FT 210..232 /label= transmembrane_domain_IV
FT 265..288 /label= transmembrane_domain_V
FT 301..323 /label= transmembrane_domain_VI
FT 301..323 /label= transmembrane_domain_VII
XX US2002103123-A1.
XX PN
XX PD
XX PD 01-AUG-2002.
XX PF 24-SEP-2001; 2001US-00962646.
XX PR 02-DEC-1994; 94US-00349025.
XX PR 01-DEC-1995; 95US-00566096.
XX PR 25-NOV-1998; 98US-00200673.
XX (SYNA-) SYNAPTIC PHARM CORP.
XX Gerald CPG, Weinshank R, Walker MW, Branchek T;
XX MPI; 2002-712388/77.
XX Modifying feeding behavior of subject, useful in treating feeding
XX disorders, involves administering to subject Y5 receptor agonist or
XX antagonist, to increase or decrease consumption of food by subject.
XX Disclosure; Fig 8A-C; 102pp; English.
XX This invention describes a novel method of modifying feeding behaviour of
XX a subject which involves administering to the subject an amount of a
XX compound which is a Y5 receptor agonist or antagonist effective to
XX increase or decrease, respectively, the consumption of food by the
XX subject so as to modify feeding behaviour of the subject. The product of
XX the invention has metabolic, anorectic, antidepressant, tranquiliser,
XX antiemetic, analgesic, hypotensive, cerebroprotective, cardiant,
XX antidiarhoeic and haemostatic activity and can be used in a vaccine. Y5
XX receptor agonist or antagonist compounds are useful for treating a
XX feeding disorder (e.g. anorexia, obesity or bulimia) in a subject. The
XX pharmaceutical compositions described in the disclosure are useful for
XX treating an abnormality alleviated by the inhibition or activation of Y5
XX receptor, in a subject. Antibodies raised against the receptor are useful
XX for detecting the presence of the receptor on the surface of a cell. The
XX agonist of Y5 receptor is useful for treating an abnormality in a
XX subject, where the abnormality includes anorexia, sexual/reproductive
XX disorder, depression, anxiety, memory loss, migraine, pain, epileptic
XX seizure, hypertension, cerebral haemorrhage, shock, congestive heart
XX failure, sleeve disturbance, nasal congestion, and diarrhoea. This
XX sequence represents the human hippocampus Y1 receptor described in the
XX disclosure of the invention
XX SQ Sequence 384 AA;
```

```
Query Match 43.8%; Score 860.5; DB 5; Length 384;
Best Local Similarity 44.9%; Pred. No. 1.9e-79;
Matches 167; Conservative 77; Mismatches 107; Indels 21; Gaps 5;
QY 16 QGENRSKPLGTPYNFSE-----HCQSDVDVMVFIVTSYSIETVVGVLNCLMC 64
Db 8 QVENHS-----VHSNFSEKKAQLLAFENDDCHLPLAMIFTLALAYGAVIILVSGNLALI 63
QY 65 VTVRQSEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFIQCMS 124
Db 64 IILKQKEMENVTNILLIWNLSFSDLLVAIMCLPLTFYITLMDHWVFGAEMCKLNPFFQCVS 123
QY 125 VTVSILSLVLVALERHOLIINPTGKPKESISOAYLIGVLIWIAVCLSLPFLANSILENVF 184
Db 124 ITVSIFSLVIAVERHOLIINPTGKPRVNNRHAYGVIAVIAVCLSLPFLIYQWTDPE 183
```



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QY 185 HKHNSKALEFLADKVVCTESWPLAHRTIYTTTLLFQYCLPLGFLVLCYARIYRLQO 244
Db 184 FQN--VTLDAYKDYKVCDFDPPSDSHRLSYTTLLVLQYFGLFCIFYFYIYRLKER 241
QY 245 GRVFKH-GTYSLRAGHKQVNVVWVAFVWLPVLFVNSLEDDHHEAIPICHGNLI 303
Db 242 NNMDKMRDNKYRSSETKRINIMLLSVVAFVWLPVLFVNSLEDDHHEAIPICHGNLI 301
QY 304 FLVCHLLAMASTCNPPIYGFINTNFKKEIKALVLTQOQSAPLESEHPLSTVHTVEVK 363
Db 302 FLCHLTAMISTCNPPIYGFINTNFKKEIKALVLTQOQSAPLESEHPLSTVHTVEVK 361
QY 364 GSLRLSGRSNPI 375
Db 362 TSLK---QASPV 370

RESULT 14
AAB14324
ID AAB14324 standard; protein; 383 AA.
XX
AC AAB14324;
XX
XX 22-NOV-2000 (first entry)
DT
DE Rhesus Y1 receptor.
XX
XX Rhesus monkey; Y1 receptor; neuropeptide Y; neurotransmitter; vasospasm;
KW heart failure, shock; cardiac hypertrophy; high blood pressure; angina;
KW myocardial infarction; sudden cardiac death; arrhythmia; renal failure;
KW peripheral vascular disease.
XX
XX Macaca mulatta.
OS
XX
XX US6087154-A.
XX
XX 11-JUL-2000.
PD
XX
XX 20-MAR-1998; 98US-00045186.
PF
XX
XX 21-MAR-1997; 97US-0041177P.
PR
XX
XX (ELIL ) LILLY & CO ELI.
DA
XX
XX Baez M, George CA;
PI
XX
XX WPI; 2000-523725/47.
DR
XX
XX N-PSDB; AAA62587, AAA62588.
DR
XX
XX Nucleic acid compound for identifying compounds for treating conditions
PT associated with excess or deficiency of neuropeptide Y encodes rhesus Y1
PT receptor which has affinity for neuropeptide Y and related peptides.
XX
XX Claim 2; Col 33-34; 21pp; English.
PS
XX
XX The present sequence is the rhesus Y1 receptor, which has affinity for
CC neuropeptide Y, pancreatic peptide and peptide YY. Neuropeptide Y is a
CC peptide present in the central and peripheral nervous systems. The
CC peptide coexists with noradrenaline in many neurons and acts as a
CC neurotransmitter alone or synergistically together with noradrenaline.
CC Neuropeptide Y interacts with a family of closely related receptors. The
CC Y1 receptor subtype appears to be the major vascular neuropeptide Y
CC receptor. The rhesus Y1 receptor is useful in identifying compounds for
CC treatment or prevention of conditions associated with an excess or
CC deficiency of neuropeptide Y. Such disorders include vasospasm, heart
CC failure, shock, cardiac hypertrophy, increased blood pressure, angina,
CC myocardial infarction, sudden cardiac death, arrhythmia, peripheral
CC vascular disease, and abnormal renal conditions such as impaired flow of
CC fluid, abnormal mass transport, or renal failure
XX
XX Sequence 383 AA;

```

```

Query Match 43.6%; Score 856.5; DB 3; Length 383;
Best Local Similarity 44.6%; Pred. No. 4.8e-79;
Matches 166; Conservative 77; Mismatches 108; Indels 21; Gaps 5;
QY 16 QGENRSKPLGTFYFNFSE-----HCQDSYDVNVFVITSYSIETVGVGLNGLCMC 64
Db 8 QVENHS-----VHSNFSEKNAQLAFENDCHLPLAMIFTLALAYGAVIILGVSGNLALII 63
QY 65 VTVQKQKAYNTNLIILANLAFSDLMCLLCOPLTAVTYTINDYMTFGETLCKSAPICOMS 124
Db 64 IILQKQKRNVTNLIILVNLSPDLVLMCLPFFVTVLMDHWVFGAMCKLNFFVQCVS 123
QY 125 VTVSILSLVALERHQLIINFTGKPSISQAYLGIVLWVACVLSLPLANSILENVF 184
Db 124 ITVSIFSLVLAVERHQLIINPRGWRPNRRHAYVGIWVLAVALSPLFIYQVWTDPE 183
QY 185 HKHNSKALEFLADKVVCTESWPLAHRTIYTTTLLFQYCLPLGFLVLCYARIYRLQO 244
Db 184 FQN--VTLDAYKDYKVCDFDPPSDSHRLSYTTLLVLQYFGLFCIFYFYIYRLKER 241
QY 245 GRVFKH-GTYSLRAGHKQVNVVWVAFVWLPVLFVNSLEDDHHEAIPICHGNLI 303
Db 242 NNMDKMRDNKYRSSETKRINIMLLSVVAFVWLPVLFVNSLEDDHHEAIPICHGNLI 301
QY 304 FLVCHLLAMASTCNPPIYGFINTNFKKEIKALVLTQOQSAPLESEHPLSTVHTVEVK 363
Db 302 FLCHLTAMISTCNPPIYGFINTNFKKEIKALVLTQOQSAPLESEHPLSTVHTVEVK 361
QY 364 GSLRLSGRSNPI 375
Db 362 TSLK---QASPV 370

RESULT 15
AAR35493
ID AAR35493 standard; protein; 384 AA.
XX
AC AAR35493;
XX
XX 25-MAR-2003 (revised)
DT 06-SEP-1993 (first entry)
XX
XX Human NPY receptor subtype Y1.
DE
XX
XX PCR; domain; primer; human; brain; neuropeptide; Y; NPY-Y1; receptor;
KW isolation; clone; fetal; NPY; probe; adult; hippocampus; cDNA library;
KW subtype Y1; cytoplasmic loop; KC; transmembrane; G protein; rat.
XX
XX Homo sapiens.
OS
XX
XX WO9309227-A1.
PN
XX
XX 13-MAY-1993.
PD
XX
XX 06-NOV-1992; 92WO-AU000600.
PF
XX
XX 06-NOV-1991; 91AU-00009336.
PR 23-JUN-1992; 92AU-00003131.
XX
XX (GARV-) GARVAN INST MEDICAL RES.
XX
XX Selbie L, Herzog H, Shine J;
XX
XX WPI; 1993-167694/20.
DR
XX
XX N-PSDB; AAQ40768.
XX
XX Human neuro-peptide Y-Y1 receptor and its DNA - useful for screening for
PT NPY agonists or antagonists.
XX
XX Disclosure; Page 8-10; 32pp; English.
XX
XX This sequence represents the human neuropeptide Y (NPY) receptor subtype
CC Y1. The cDNA encoding this sequence was isolated from human fetal brain

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OM protein - protein search, using sw model

Run on: May 11, 2004, 12:50:37 ; Search time 21 Seconds
(without alignments)
1717.706 Million cell updates/sec

Title: US-09-430-775-2
Perfect score: 1965
Sequence: 1 MNTSHLLALLPKSPQGENR.....TVTEVSKGSLRSGRSNPI 375

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1965	100.0	375	2 139182	neuropeptide Y/pep
2	1962	99.8	375	2 G02300	pancreatic polypep
3	1519	77.3	375	2 S63685	neuropeptide Y rec
4	869	44.2	382	2 B45133	neuropeptide Y/pep
5	867	44.1	382	2 S23788	neuropeptide Y rec
6	856.5	43.6	384	2 A45490	neuropeptide Y/pep
7	823	41.9	366	2 S71152	neuropeptide Y/pep
8	822.5	41.9	349	2 S12863	G protein-coupled
9	483	24.6	370	1 I52315	neuropeptide Y/pep
10	468	23.8	381	2 I39187	neuropeptide Y/pep
11	430	21.9	423	2 B40470	glucocorticoid-ind
12	410	20.9	443	2 D40470	glucocorticoid-ind
13	395	20.1	455	2 T15622	hypothetical prote
14	387	19.7	491	2 C40470	glucocorticoid-ind
15	381.5	19.4	457	2 T29741	hypothetical prote
16	378.5	19.3	391	2 T32714	hypothetical prote
17	370.5	18.9	399	2 A46632	bombesin-like pept
18	368.5	18.8	394	2 J07209	galanin receptor -
19	366	18.6	384	2 A39003	bombesin/gastrin-r
20	364	18.5	365	2 T20184	hypothetical prote
21	363	18.5	384	2 I57682	bombesin/ GRP rece
22	359	18.3	349	2 I59336	galanin receptor 1
23	358.5	18.2	399	2 S29480	bombesin receptor
24	357.5	18.2	384	2 A41007	gastrin-releasing
25	356	18.1	449	2 A41738	neuropeptide Y rec
26	345.5	17.6	376	2 I50102	Phel3 bombesin rec
27	339.5	17.3	412	2 T22076	hypothetical prote
28	337	17.2	357	2 J07319	probable allatosta
29	337	17.2	423	2 J07677	allatostatin recep

30	330.5	16.8	390	2 JH0374	bombesin receptor,
31	327	16.6	447	2 A47430	gastrin/cholecysto
32	326	16.6	444	2 A42685	cholecystokinin re
33	326	16.6	453	2 S32817	gastrin receptor -
34	326	16.6	584	2 J07809	sulfakinin recepto
35	325.5	16.6	371	2 J05796	probable chemoattr
36	325	16.5	427	2 S50150	gastric CCK-A rece
37	324.5	16.5	371	2 J05498	G protein-coupled
38	323	16.4	440	2 A44081	kappa-type opioid
39	323	16.4	539	2 T27559	hypothetical prote
40	321.5	16.4	428	2 JN0692	cholecystokinin ty
41	321.5	16.4	436	2 J05599	cholecystokinin-A
42	321	16.3	465	1 J01517	neurokinin 3 recep
43	320	16.3	385	2 S55524	neurokinin 3 recep
44	320	16.3	430	2 I51898	cholecystokinin-A
45	320	16.3	452	2 A34916	neurokinin 3 recep

ALIGNMENTS

RESULT 1

139182
neuropeptide Y/peptide YY receptor Y4 - human
C;Species: Homo sapiens (man)
C;Date: 01-Mar-1996 #sequence_revision 01-Mar-1996 #text_change 20-Apr-2000
C;Accession: I39182
R;Bard, J.A.; Walker, M.W.; Branchek, T.A.; Weinshank, R.L.
J. Biol. Chem. 270, 26762-26765, 1995
A;Title: Cloning and functional expression of a human Y4 subtype receptor for pancreatic
C;Reference number: I39182; MUID:96070761; PMID:7592911
A;Accession: I39182
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-375 <RES>
A;Cross-references: EMBL:U35232; NID:G1063629; PIDN:NAC50280.1; PID:G1063630
C;Superfamily: neurokinin 1 receptor
C;Keywords: appetite

Query Match 100.0%; Score 1965; DB 2; Length 375;
Best Local Similarity 100.0%; Pred. No. 2.1e-161;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNTSHLLALLPKSPQGENRKPGLTPYNFSEHCQSDVDMVFIVTSYSIETVGVGLNL	60
Db	1	MNTSHLLALLPKSPQGENRKPGLTPYNFSEHCQSDVDMVFIVTSYSIETVGVGLNL	60
Qy	61	CLMCVTVRQKERANVTNLLIANLAFSDFLMCLLCQPLTAVYIMDYWIFGETLCKMSAFI	120
Db	61	CLMCVTVRQKERANVTNLLIANLAFSDFLMCLLCQPLTAVYIMDYWIFGETLCKMSAFI	120
Qy	121	QCMSTVTSILSVLVAERHQLIINPTGKPKSIQAYLGIVLIWVIACVLSLPLANSIL	180
Db	121	QCMSTVTSILSVLVAERHQLIINPTGKPKSIQAYLGIVLIWVIACVLSLPLANSIL	180
Qy	181	ENVFHNKHSKALEFLADKVVCTESWPLAHRITTYTFFLLFOYCLPLGFILVCYARIYR	240
Db	181	ENVFHNKHSKALEFLADKVVCTESWPLAHRITTYTFFLLFOYCLPLGFILVCYARIYR	240
Qy	241	LQRCGRVFHKGTYSLRAGHKQNVVNVVAVFVWLPLHVFNSLEDWHHEAIPICHG	300
Db	241	LQRCGRVFHKGTYSLRAGHKQNVVNVVAVFVWLPLHVFNSLEDWHHEAIPICHG	300
Qy	301	NLFLVCHLLAMASTCVNPFYGFNTNPKETKALVLTCCQSAPLESEHPLSLVTHTE	360
Db	301	NLFLVCHLLAMASTCVNPFYGFNTNPKETKALVLTCCQSAPLESEHPLSLVTHTE	360
Qy	361	VSKGSLRLSGRSNPI	375
Db	361	VSKGSLRLSGRSNPI	375

RESULT 2

G02300

pancreatic polypeptide receptor - human

C:Species: Homo sapiens (man)

C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 20-Apr-2000

C:Accession: G02300

R:Yan, H.; Yang, J.; Marasco, J.; Yamaguchi, K.; Brenner, S.; Collins, F.; Karbon, W.

submitted to the EMBL Data Library, December 1995

A:Reference number: H01018

A:Accession: G02300

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-375 <YAN>

A:Cross-references: EMBL:U42387; NID:g1314327; PIDN:AAB07759.1; PID:g1314328

C:Superfamily: neurokinin 1 receptor

Query Match 99.8%; Score 1962; DB 2; Length 375;

Best Local Similarity 99.7%; Pred. No. 3.8e-161;

Matches 374; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNTSHLLALLPKSPQGENRSKPLGTPYNSFSEHCQSDVDVMVFIVTSYSIETVVGVLGNL 60

Db 1 MNTSHLLALLPKSPQGENRSKPLGTPYNSFSEHCQSDVDVMVFIVTSYSIETVVGVLGNL 60

Qy 61 CLMCVTVROKESKANVTNLLIANLAFSDFLMCLLCQPLTAVTITMDYIFGTELCRMSAFI 120

Db 61 CLMCVTVROKESKANVTNLLIANLAFSDFLMCLLCQPLTAVTITMDYIFGTELCRMSAFI 120

Qy 121 QCMSVTVSILSLVALERHQLINPTGWKPSISOAYLGIVLIWIAVCVLSLPLANSIL 180

Db 121 QCMSVTVSILSLVALERHQLINPTGWKPSISOAYLGIVLIWIAVCVLSLPLANSIL 180

Qy 181 ENVFPHKHSKALFLADKVVCTESWPLAHRHTITFTFLFOYCLPLGFLVCVARIYR 240

Db 181 ENVFPHKHSKALFLADKVVCTESWPLAHRHTITFTFLFOYCLPLGFLVCVARIYR 240

Qy 241 LQQRGVFHKGTSYSLRAGHKQNVVLMVAVAFVLMPLHVFNSLEDWHHEAIPICHG 300

Db 241 LQQRGVFHKGTSYSLRAGHKQNVVLMVAVAFVLMPLHVFNSLEDWHHEAIPICHG 300

Qy 301 NLIFLVCHLLAMASTCNPPIYGFINTNPKETKALVLTCCQSAPLSESHLPLSTVHTE 360

Db 301 NLIFLVCHLLAMASTCNPPIYGFINTNPKETKALVLTCCQSAPLSESHLPLSTVHTE 360

Qy 361 VSKGSLRLSGRSNPI 375

Db 361 VSKGSLRLSGRSNPI 375

RESULT 3

S63685

neuropeptide Y receptor D type - mouse

C:Species: Mus musculus (house mouse)

C:Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 20-Apr-2000

C:Accession: S63685

R:Gregor, P.; Millham, M.L.; Feng, Y.; DeCarr, L.B.; McCaleb, M.L.; Cornfield, L.J.

FEBS Lett. 381, 58-62, 1996

A:Title: Cloning and characterization of a novel receptor to pancreatic polypeptide, a

A:Reference number: S63685; MUID:96193913; PMID:8641440

A:Accession: S63685

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-375 <GRE>

A:Cross-references: EMBL:U40189; NID:g1223969; PIDN:AAC52442.1; PID:g1223970

C:Superfamily: neurokinin 1 receptor

Query Match

Best Local Similarity 77.3%; Score 1519; DB 2; Length 375;

Matches 283; Conservative 35; Mismatches 55; Indels 0; Gaps 0;

Qy 1 MNTSHLLALLPKSPQGENRSKPLGTPYNSFSEHCQSDVDVMVFIVTSYSIETVVGVLGNL 60

Db 1 MNTSHLLALLPKSPQGENRSKPLGTPYNSFSEHCQSDVDVMVFIVTSYSIETVVGVLGNL 60

Qy 61 CLMCVTVROKESKANVTNLLIANLAFSDFLMCLLCQPLTAVTITMDYIFGTELCRMSAFI 120
Db 61 CLFVTVTRQEKSNVTNLLIANLAFSDFLMCLLCQPLTAVTITMDYIFGTELCRMSAFI 120

Qy 121 QCMSVTVSILSLVALERHQLINPTGWKPSISOAYLGIVLIWIAVCVLSLPLANSIL 180
Db 121 QCMSVTVSILSLVALERHQLINPTGWKPSISOAYLGIVLIWIAVCVLSLPLANSIL 180

Qy 181 ENVFPHKHSKALFLADKVVCTESWPLAHRHTITFTFLFOYCLPLGFLVCVARIYR 240
Db 181 NDLFPHYNSKVVEFLDKVVCFVSWSDHRLITFTFLFOYCLPLAFIVCYIRIYR 240

Qy 241 LQQRGVFHKGTSYSLRAGHKQNVVLMVAVAFVLMPLHVFNSLEDWHHEAIPICHG 300
Db 241 LQQRGVFHAFACSSRAGQMKRINSMLMTMTVAFVLMPLHVFNTLEDWYQEAIPACHG 300

Qy 301 NLIFLVCHLLAMASTCNPPIYGFINTNPKETKALVLTCCQSAPLSESHLPLSTVHTE 360
Db 301 NLIFLVCHLLAMASTCNPPIYGFINTNPKETKALVLTCHCRSPQSESEHPLSTVHTE 360

Qy 361 VSKGSLRLSGRSN 373
Db 361 LSKGSMEMGSKSN 373

RESULT 4

B46133

neuropeptide Y/peptide YY receptor Y1 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Apr-2000

C:Accession: B46133

R:Herzog, H.; Hort, Y.J.; Ball, H.J.; Hayes, G.; Shine, J.; Selbie, L.A.

Proc. Natl. Acad. Sci. U.S.A. 89, 5794-5798, 1992

A:Title: Cloned human neuropeptide Y receptor couples to two different second messenger s

A:Reference number: A46133; MUID:92335184; PMID:1321422

A:Accession: B46133

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-382 <HER>

A:Note: sequence extracted from NCBI backbone (NCBIP:108539)

C:Superfamily: neurokinin 1 receptor

C:Keywords: appetite; G protein-coupled receptor; transmembrane protein

Query Match

Best Local Similarity 44.2%; Score 869; DB 2; Length 382;

Matches 168; Conservative 74; Mismatches 101; Indels 16; Gaps 4;

Qy 28 YNFSBH-----CQSDVDVMVFIVTSYSIETVVGVLNCLMCVTVROKESKANVTN 77

Db 16 YNVSNGPFLAFENDDCFLPLAVITLALAYGAVIILGVSGNLALIIILKQKEMRNVN 75

Qy 78 LLIANLAFSDFLMCLLCQPLTAVTITMDYIFGTELCRMSAFIQCMSVTVSILSLVAL 137

Db 76 ILIVNLSFDLLVAVMCLPFTFVYTLMDHNVFGETMCKLNPFCVSIYISFLVLI 135

Qy 138 ERHQLINPTGWKPSISOAYLGIVLIWIAVCVLSLPLANSILNVHFKHKSALFLAD 197

Db 136 ERHQLINPTGWKPSISOAYLGIVLIWIAVCVLSLPLANSILNVHFKHKSALFLAD 193

Qy 198 KVCTESWPLAHRHTITFTFLFOYCLPLGFLVCVARIYRRLQGRVHFHKGTSY-LR 256

Db 194 KVCFDEKPSDSHLSLSTLLVLYQYFGLCFYCFYKLYIRLKRNNMMDKIRDSKYR 253

Qy 257 AGHKQNVVLMVAVAFVLMPLHVFNSLEDWHHEAIPICHGNIPLVCHLLAMASTC 316

Db 254 SSETKRINWMLLSVAVAFVAVCKLPLTIFNTVFDWNHQLIATCNENLLFLCHLTAMSTC 313

Qy 317 VNPFTYGFINTNPKETKALVLTCCQSAPLSESHLPLSTVHTEVSKGSLRLSGRSNPI 375

Db 314 VNPFTYGFINTNPKETKALVLTCCQSAPLSESHLPLSTVHTEVSKGSLRLSGRSNPI 369

RESULT 5

S27388
neuropeptide Y receptor NPV-1 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Apr-2000
C:Accession: S27388
R;Eva, C.; Oberto, A.; Sprengel, R.; Genazzani, E.
FEBS Lett. 314, 285-288, 1992
A:Title: The murine NPV-1 receptor gene. Structure and delineation of tissue-specific exons
A:Reference number: S27388; MUID:93106169; PMID:1468559
A:Accession: S27388
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-382 <EVA>
A:Cross-references: EMBL:Z18280; NID:953438; PIDN:CAA9157.1; PID:953439
C:Superfamily: neurokinin 1 receptor

Query Match 46.1%; Score 867; DB 2; Length 382;
Best Local Similarity 46.5%; Pred. No. 6e-67;
Matches 167; Conservative 75; Mismatches 101; Indels 16; Gaps 4;

QY 28 YNFSEH-----QDSVDVMVFIVTSYISIVTGVGLNCLMCMVTVRQEKANVTN 77
DB 16 YNASENSPLAFENDCHLPIAVITFTLALAYGAVIILGVSGNLALIIILKQEMRNVTN 75

QY 78 LLIANLAFSDFLMCLLCOPLTAVTMDYIMFGETLCKMGAFIQCMSTVTSILSLVAL 137
DB 76 ILIIVNLSFSDLLVAVMCLPFTFTVTLMDHWVFGETMCKLNPFFVQCVSIITVTSISLVLIIV 135

QY 138 ERHQLIINPTGKPSISOAYLGIVLWVIAVCLVSLPLANSILENVFHKNSKALEFLAD 197
DB 136 ERHQLIINPRGWRPNRHHAYIGITVIVWLVAVASSLPFVIYQILTDEPFQNVLS--LAAPKD 193

QY 198 KVVCTESPLAHHRTIYTTLLFOYCLPLGLFVLVAVVIRYRRLQGRGVFHKGTYS-LR 256
DB 194 KYVCFDKPSSSHRLSYTYLLLVLYQYFGPLCFIFCYFKYIRUKRRNMWDKIRDSKYR 253

QY 257 AGHKQNVNVLVWVAVAFVAVLWPLHVNLSLWHEAIPICHGNLIPLVCHLLAMASTC 316
DB 254 SSETKRINIMLLSVAVAFVAVCWLPITFTNTVDNHHQIATCNHNLPLFLCHLTAMISTC 313

QY 317 VNPFIYGLNTNFKEIKALVLTQOSAPLESSEHLPLSTVHTVSKSLRSLSRNP 375
DB 314 VNPFIYGLNKNFORDLFFNFCDFRSDDDYETIAMSTWHTDVSLSLK--QASPV 369

RESULT 6
A45490
neuropeptide Y/peptide YY receptor Y1 - human
C:Species: Homo sapiens (man)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Apr-2000
C:Accession: A45490; A46133; A42773
R;Herzog, H.; Baumgartner, M.; Vivero, C.; Selbie, L.A.; Auer, B.; Shine, J.
J. Biol. Chem. 268, 6703-6707, 1993
A:Title: Genomic organization, localization, and allelic differences in the gene for the Y1 receptor
A:Reference number: A45490; MUID:93203272; PMID:8095935
A:Accession: A45490
A:Molecule type: DNA
A:Residues: 1-384 <HER>
A:Cross-references: GB:L07615; NID:G189284; PIDN:AAA59947.1; PID:G189285
A:Note: sequence extracted from NCBI backbone (NCBIN:128005, NCBIIP:128000)
R;Herzog, H.; Hort, Y.J.; Ball, H.J.; Hayes, G.; Shine, J.; Selbie, L.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 5794-5798, 1992
A:Title: Cloned human neuropeptide Y receptor couples to two different second messenger systems
A:Reference number: A46133; MUID:92335184; PMID:1321422
A:Accession: A46133
A:Status: preliminary
A:Molecule type: mRNA
A:Notes: sequence extracted from NCBI backbone (NCBIIP:108538)
R;Larhammar, D.; Blomqvist, A.G.; Yee, F.; Jazin, E.; Yoo, H.; Wahlested, C.
J. Biol. Chem. 267, 10935-10938, 1992
A:Title: Cloning and functional expression of a human neuropeptide Y/peptide YY receptor
A:Reference number: A42773; MUID:92283782; PMID:1317848

A:Accession: A42773
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-384 <LAR>
A:Cross-references: GB:M89461; NID:G189155; PIDN:AAA73215.1; PID:G189156
A:Experimental source: fetal brain
A:Note: sequence extracted from NCBI backbone (NCBIN:104735, NCBIIP:104736)
C:Genetics:
A:Gene: GDB:NPY1R; NPYR
A:Cross-references: GDB:132643; OMIM:162641
A:Map position: 4q31.3-4q32
C:Superfamily: neurokinin 1 receptor
C:Keywords: appetite; G protein-coupled receptor; glycoprotein; lipoprotein; thiolester
F;37-66/Domain: transmembrane #status predicted <TM1>
F;77-103/Domain: transmembrane #status predicted <TM2>
F;118-136/Domain: transmembrane #status predicted <TM3>
F;155-179/Domain: transmembrane #status predicted <TM4>
F;209-232/Domain: transmembrane #status predicted <TM5>
F;261-286/Domain: transmembrane #status predicted <TM6>
F;300-323/Domain: transmembrane #status predicted <TM7>
F;313-198/Disulfide bonds: #status predicted
F;186/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;338/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 43.6%; Score 856.5; DB 2; Length 384;
Best Local Similarity 44.6%; Pred. No. 4.8e-66;
Matches 166; Conservative 77; Mismatches 108; Indels 21; Gaps 5;

QY 16 QENRSKPLGTPTNFSE-----HCQDSVDVMVFIVTSYISIVTGVGLNCLMC 64
DB 8 QVENHS-----VHSNFSKNAQLAFENDCHLPIAVITFTLALAYGAVIILGVSGNLALII 63

QY 65 VTVROKEKANVTNLIANLAFSDFLMCLLCOPLTAVTMDYIMFGETLCKMGAFIQCMS 124
DB 64 IILKQEMRNVTNLIIVNLSFSDLLVAVMCLPFTFTVTLMDHWVFGEMCKLNPFFVQCVS 123

QY 125 VTVSILSLVVALERHQLIINPTGKPSISOAYLGIVLWVIAVCLVSLPLANSILENVF 184
DB 124 ITVSFSLVLIIVERHQLIINPRGWRPNRHHAYIGITVIVWLVAVASSLPFVIYQVMTDEP 183

QY 185 KHNHSALEFLADKVVCTESPLAHHRTIYTTLLFOYCLPLGLFVLVAVVIRYRRLQGR 244
DB 184 FQN--VTLDAYKDKVYCFQDFSDSHRLSYTYLLLVLYQYFGPLCFIFCYFKYIRUKRR 241

QY 245 GRVFXH-GTYSLRAGHKQNVNVLVWVAVAFVAVLWPLHVNLSLWHEAIPICHGNLI 303
DB 242 NNMDKVRDNKYRSSETKRINIMLLSVAVAFVAVCWLPITFTNTVDNHHQIATCNHNL 301

QY 304 FLVCHLLAMASTCVNPFYGLNTNFKEIKALVLTQOSAPLESSEHLPLSTVHTVSK 363
DB 302 FLCHLLTAMISTCVNPFYGLNKNFORDLFFNFCDFRSDDDYETIAMSTWHTDVS 361

QY 364 GSLRLSGRNP 375
DB 362 TSLK--QASPV 370

RESULT 7
S71152
neuropeptide Y/peptide YY receptor Y1 - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 27-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Apr-2000
C:Accession: S71152; S55924
R;Martens, G.J.; Blomqvist, A.G.; Roubos, E.W.; Larhammar, D.
submitted to the EMBL Data Library, November 1993
A:Description: Cloning and sequencing of an neuropeptide Y/peptide YY receptor from Xenopus
A:Reference number: S71152
A:Accession: S71152
A:Molecule type: mRNA
A:Residues: 1-366 <MAR>
A:Cross-references: EMBL:L25416; NID:G409169; PIDN:AAA49918.1; PID:G409170
A:Experimental source: brain, hypothalamus
R;Blomqvist, A.G.; Roubos, E.W.; Larhammar, D.; Martens, G.J.M.

Biochim. Biophys. Acta 1261, 439-441, 1995
A;Title: Cloning and sequence analysis of a neuropeptide Y/peptide YY receptor Y1 cDNA
A;Reference number: S55924; MUID:95260870; PMID:7742373
A;Accession: S55924
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-278; I: 280-366 <BIO>
A;Cross-references: EMBL:L25416; NID:9409169
C;Superfamily: neurokinin 1 receptor
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 41.9%; Score 823; DB 2; Length 366;
Best Local Similarity 44.4%; Pred. No. 3.5e-63;
Matches 161; Conservative 71; Mismatches 121; Indels 10; Gaps 4;

QY 18 ENRSKPLGTPYN----PSEHCDSVDVMVFIVTSYIETWVGVLNCLMCMVTVRQKEKA 73
DB 8 ENLSVFNISGNITFPISDCALPLPMIPTLALAYGAVIILGSLNALIILKQKMR 67
QY 74 NVTNLALANAFSDFMLCLLCOPLTAVTMDYIMWIFETLCKMSAFIOCMSTVTSLSIV 133
DB 68 NVTNLIIVNLSFDLLATINCLPFTIYIMDMHWIFGEVWCKNEVIQCVSVTVSIFSLV 127
QY 134 LVALERHQLIINPTGKPSIQAYLGIVLIWIAVCVLSLPLANSILENVFHNHSHKALE 193
DB 128 LIAIERHQLIINPRGWRPNRHACFGITWIGPAMACSTPLMYSVLTDPEPKNIS--LD 185
QY 194 FLADKVCVETSWPLAHHRTIYTTFFLLFOYCLPLGILVCIYARIYRRLQROGRVPHK-GT 252
DB 186 SYTGKVCVLEDFEDKFRSLYTTLLFILOYLGLPCFIFVCYTKIFLRLKRNMDKIRD 245
QY 253 YSLRAGHKQNVVLMVAVAFVLPVLFVFNLSLEDWHEAIPICHGNLIPLVCHLLAM 312
DB 246 NKYSRSTKRNIMLLSIVVGFALCWLPPFIPNLVFNWHEAVATCNHLLFLICHTAM 305
QY 313 ASTCVNPPYVGLNTWPKKEIKALVLTQOSAPLESEHLPSTVHTVEKSLRSGRS 372
DB 306 ISTCVNPIFYGLNFQNFORDLOFPFFNFCDFRSREDDYETIAMTMTDYSKSLK---QA 362
QY 373 NPI 375
DB 363 SPI 365

RESULT 8
S12863
G protein-coupled receptor FC5 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 20-Apr-2000
C;Accession: S12863; S19101
R;Eva, C.; Keinaenen, K.; Monyer, H.; Seeburg, P.; Sprengel, R.
FEBS Lett. 271, 81-84, 1990
A;Title: Molecular cloning of a novel G protein-coupled receptor that may belong to the
A;Reference number: S12863; MUID:91032093; PMID:2172008
A;Accession: S12863
A;Molecule type: mRNA
A;Residues: 1-349 <EVA>
A;Cross-references: EMBL:Z11504
R;Krause, J.; Eva, C.; Seeburg, P.; Sprengel, R.
submitted to the EMBL Data Library, November 1991
A;Description: Pharmacological and Transduction Properties of a Recombinantly Expressed
A;Reference number: S19101
A;Accession: S19101
A;Molecule type: mRNA
A;Residues: 1-343; 'DYETINMTMTDYSKSLKQASPAVKKISMNDNEKI' <KRA>
A;Cross-references: EMBL:Z11504; NID:957636; PIDN:CAA7579.1; PID:957637
C;Superfamily: neurokinin 1 receptor
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
F;39-61/Domain: transmembrane #status predicted <TM1>
F;73-93/Domain: transmembrane #status predicted <TM2>
F;114-135/Domain: transmembrane #status predicted <TM3>
F;155-175/Domain: transmembrane #status predicted <TM4>
F;213-231/Domain: transmembrane #status predicted <TM5>

F;262-285/Domain: transmembrane #status predicted <TM6>
F;299-322/Domain: transmembrane #status predicted <TM7>
F;2,11,17/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;346/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 41.9%; Score 822.5; DB 2; Length 349;
Best Local Similarity 48.5%; Pred. No. 3.6e-63;
Matches 157; Conservative 62; Mismatches 92; Indels 13; Gaps 3;

QY 28 YNFSEH-----CODSDVMVFIVTSYIETWVGVLNCLMCMVTVRQKEKANVTN 77
DB 16 YNVSESPFLAFENDCHFLPVLAVIFTLALAYGAVIILGVSGLNALIILKQKMRNVTN 75
QY 78 LLIANLAFSPFLMCLLCOPLTAVTMDYIMWIFETLCKMSAFIOCMSTVTSLSIVLVAL 137
DB 76 ILIYNLSFDLLAVMCLPFTIYIMDMHWIFGEVWCKNEVIQCVSVTVSIFSLVLI 135
QY 138 ERHQLIINPTGKPSIQAYLGIVLIWIAVCVLSLPLANSILENVFHNHSHKALEPLAD 197
DB 136 ERHQLIINPRGWRPNRHACFGITWIGPAMACSTPLMYSVLTDPEPKNIS--LA 193
QY 198 KVCETSWPLAHHRTIYTTFFLLFOYCLPLGILVCIYARIYRRLQROGRVPHKGTYS-LR 256
DB 194 KYVCFDKPDSHRSLSYTTLLVLQYFGPLCFICFYKTIYIRLKRNNMDKIRDSKYR 253
QY 257 AGHKQNVVLMVAVAFVLPVLFVFNLSLEDWHEAIPICHGNLIPLVCHLLAMASTC 316
DB 254 SSETKRNIMLLSIVVAFVLCWLPPFIPNLVFNWHEAVATCNHLLFLICHTAM 313
QY 317 VNPTFYGLNTWPKKEIKALVLT 340
DB 314 VNPIFYGLNKNFORDLOQFFNF 337

RESULT 9
I52315
G protein-coupled receptor UHR-1 - rat
C;Species: Rattus sp. (rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-May-2000
C;Accession: I52315
R;Welch, S.K.; O'Hara, B.F.; Kilduff, T.S.; Heller, H.C.
Biochem. Biophys. Res. Commun. 209, 606-613, 1995
A;Title: Sequence and tissue distribution of a candidate G-coupled receptor cloned from
A;Reference number: I52315; MUID:95251659; PMID:7733930
A;Accession: I52315
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-370 <RES>
A;Cross-references: GB:S77867; NID:9988527; PIDN:ABE34129.1; PID:9988528
C;Superfamily: neurokinin 1 receptor

Query Match 24.6%; Score 483; DB 1; Length 370;
Best Local Similarity 35.7%; Pred. No. 6.2e-34;
Matches 129; Conservative 59; Mismatches 129; Indels 44; Gaps 12;

QY 11 LPKSPQGE---NRSKPLG-TPYNFS-EHCODSDVMV-----FI 44
DB 4 LPQGTGDPDLFGSPAGSTPANQSAESENVSATVPRAAAVTPQSLVHLQKGLI 63
QY 45 VTSYIETWVGVLNCLMCMVTVRQKEKANVTNLIANLAFSDFLMCLLCOPLTAVTITM 104
DB 64 VMLYSIVVVGVLGNCCLLVLIARVRLHNVTNFIIGNLALSDVLWCAACVPLTLAYAFE 123
QY 105 DY-WIFGETLCKMSAFIOCMSTVTSLSIVLVALERHQLIINPTGKPSISQAYLGIVLI 163
DB 124 PRGWFGGGLCHLVFFLQPVTVVSVFTLTIAVDVRLVHLPLRRISLKSAYAVLGI 183
QY 164 VWIACVLSLPLANSILENVFHNHSHKALEPLADKVCVETSW-PLAHHRTIYTTFFLLFQ 222
DB 184 WALSAVLALPAVHTY--HVELKPH-----DVRICEEPWGSQERQRIYANGLLGT 233
QY 223 YCLPLGFLVCIYARIYRRLQRO---GRVFHKGTYSLRAGHKQNVVLMVAVAFVWL 279

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Db 234 YLLPLLAIIILSYRVSVKLRNRVPGSVTQSQADMDRA-RRRTFTCLLVVVVVVFALCWL 292
QY 280 PLHVFNSLEWHHEAI-PICHGNLIPLVCHLLAMASTCVNPFYIGFINTNFKKEIKALVL 338
Db 293 PLHFNLRDLDRADIPAFG-LVQLCHLWASSACYNPFYIYAWLHDSFREELRKMIL 351
QY 339 T 339
Db 352 S 352

RESULT 10
139187
neuropeptide Y/peptide YY receptor Y2 - human
N:Alternate names: neuropeptide Y/peptide YY receptor type 2
C:Species: Homo sapiens (man)
C:Date: 01-Mar-1996 #sequence_revision 01-Mar-1996 #text_change 20-Apr-2000
C:Accession: I39187; I39163; G02301
R:Gerald, C.; Walker, M.W.; Vayesse, P.J.
J. Biol. Chem. 270, 26758-26761, 1995
A:Title: Expression cloning and pharmacological characterization of a human hippocampal
A:Reference number: I39187; MUID:96070760; PMID:7592910
A:Accession: I39187
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-381 <GER>
A:Cross-references: EMBL:U36269; NID:gl063633; PIDN:AA050281.1; PID:gl063634
R:Rose, P.M.; Fernandes, P.; Lynch, J.S.; Frazier, S.T.; Fisher, S.M.; Kodukula, K.; Kie
J. Biol. Chem. 270, 22661-22664, 1995
A:Title: Cloning and functional expression of a cDNA encoding a human type 2 neuropeptid
A:Reference number: I39163; MUID:96032678; PMID:7559383
A:Accession: I39163
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-133, 'A', 135-381 <ROS>
A:Cross-references: EMBL:U32500; NID:gl000750; PIDN:AAA93170.1; PID:gl000751
R:Yan, H.; Yang, J.; Marasco, J.; Yamaguchi, K.; Brenner, S.; Collins, F.; Karbon, W.
submitted to the EMBL Data Library, December 1995
A:Reference number: H01019
A:Accession: G02301
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-171, 'G', 173, 'R', 175-201, 'P', 203-208, 'A', 210-381 <YAN>
A:Cross-references: EMBL:U42389; NID:gl134329; PIDN:AA07760.1; PID:gl134330
C:Genetics:
A:Gene: GDB:NPV29
A:Cross-references: GDB:4365607; OMIM:162642
A:Map position: 4q31-q31
C:Superfamily: neurokinin 1 receptor
C:Keywords: appetite; G protein-coupled receptor; glycoprotein; lipoprotein; thiolester
F:49-76/Domain: transmembrane #status predicted <TM1>
F:87-113/Domain: transmembrane #status predicted <TM2>
F:166-186/Domain: transmembrane #status predicted <TM4>
F:221-237/Domain: transmembrane #status predicted <TM5>
F:269-291/Domain: transmembrane #status predicted <TM6>
F:305-328/Domain: transmembrane #status predicted <TM7>
F:123-203/Disulfide bonds: #status predicted
F:342/Binding site: palmitate (Cys) (covalent) #status predicted
F:372/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 23.8%; Score 458; DB 2; Length 381;
Best Local Similarity 32.5%; Pred. No. 1.2e-32;
Matches 115; Conservative 66; Mismatches 12; Indels 46; Gaps 9;

QY 38 VDWMVFIVTSYGIETVVGVLNCLMCTVTRQKEXANTVNLIANLAFSDFLMLCCOPL 97
Db 47 IEVQVVLILAYCSIIILGVIGNSLVIVHVIKFSNRTVTNFFIANLAVADLLVNTLCILPF 106
QY 98 TAVYIMDVIWGEITLCKNSAFIQMSVTSLSLVALSRHQLINPTGKPSISQAY 157
Db 107 TLTITLMGKWKGPVLCHLVPQAQGLAVQSVTITLALDRHRCIVLHLSKSKIRISF 166
QY 158 LGIVLIWVIACVLSLP---FLANSILENVFHNKNSKALEFLADKVCTESWP---LAHRH 211
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Db 167 LTIIGLAWGISALLASPLAIFREYSLEII---PDF--EIVACTEKWPGEEKSIYG 216
QY 212 TTYTTFLLLFQVCLPLGLFVLCYARIYERLORQ-----GRVFHKGTYSLRAGHKQVNV 265
Db 217 TVISLSSLLILVPLGLIISFSYTRISKLKNHVSFGANDHYHQ-----RRQKTK 268
QY 266 VLVVMVAFVAVLWLPPLHVFNSLEDWHHEAIPICHGNLIPLVCHLLAMASTCVNPFYIGFL 325
Db 269 MLVGVVVVFAVSWLPPLHAFQLAVIDSQVLDLKEYKLIFTVFHIIAMGTTANPLLYGM 328
QY 326 NTNFKKEIKALVLTQOSAPLESEHPLSLSTVHTVS-----KGSRLSLSGRSNP 374
Db 329 NSNYRKAFLS-APRCEQR-----LDAIHSEVSVTFKAKCNLEVRKNSGP 371

RESULT 11
B40470
glucocorticoid-induced receptor precursor, short form RP23 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 20-Apr-2000
C:Accession: B40470
R:Harrigan, M.T.; Campbell, N.F.; Bourgeois, S.
Mol. Endocrinol. 5, 1331-1338, 1991
A:Title: Identification of a gene induced by glucocorticoids in murine T-cells: a potent
A:Reference number: A40470; MUID:92123228; PMID:1663214
A:Accession: B40470
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-423 <HAR>
A:Cross-references: GB:M80481; GB:M80610; NID:gl193516; PIDN:AAA17882.1; PID:gl460318
C:Superfamily: neurokinin 1 receptor

Query Match 21.9%; Score 430; DB 2; Length 423;
Best Local Similarity 32.4%; Pred. No. 2.6e-29;
Matches 121; Conservative 68; Mismatches 142; Indels 42; Gaps 12;

QY 17 GENRSKPLGTPYNFSSHCDQSV-----DVMVFIVTSYSIETVVGVLNCLMC 64
Db 36 GPNASSHFWANYTFSD-WQNFVGRRRYGAESQNPVKALLIVAYSPTIVSLFGNVLVCH 94
QY 65 VTVRQKEKANVTMLIANLAFSDPLMLCLOPLTAVYIMDYIMTDFGETLCKNSAFIQMS 124
Db 95 VIFKNQRMHSATSLFIWNLAVADIMTLTNPFTLVFVNSTWVFGKGMCHVSRRFAQYCS 154
QY 125 VTVSILSLVLVALERHOLIINPTGKPSISOAYGLGIVLIWVIACVLSLPLFLANSILENVF 184
Db 155 LHVSALTILTAIADVDRHOVIMHPLKPRISITKGVIIYIAVWVATFSLP---HAICQKLF 211
QY 185 HKNHSALEFLADKVCTESWP-----LAHRITYTTFLLFQVCLPLGLFVLCYARIYR 240
Db 212 TFKYSEDIV-----RSLCLPDFPEPADLFWKYLDTATFILL--YLLPLFTISVAYARVAKK 265
QY 241 L---QRQGRVFHKGTYSLRAGHKQVNV-VLVVMVAFVAVLWLPPLHVFNSLEDWHHEAIP 296
Db 266 LMLCNTIGDVTEQYLALR--RKKTTVKMLVLVWVLPALCHFFPLNCYVLL-----LSSKA 319
QY 297 ICHGNLIPLVCHLLAMASTCVNPFYIGFINTNFKKEIKALVLTQOSAPLESEHPL--- 353
Db 320 IHTNNALYFAHFWAFMSSTCYNPFYICWLNENFRVELKALLSMCOR-PPKPOEDRLPSVP 378
QY 354 --LSTVHTVSCKG 364
Db 379 PSFVAVTEKSHG 391

RESULT 12
D40470
glucocorticoid-induced receptor, long form RP105 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 20-Apr-2000
C:Accession: B40470
R:Harrigan, M.T.; Campbell, N.F.; Bourgeois, S.
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Mol. Endocrinol. 5, 1331-1338, 1991
A:Title: Identification of a gene induced by glucocorticoids in murine T-cells: a potent
A:Reference number: A40470; MUID:92123228; PMID:1663214
A:Accession: D40470
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-443 <HAR>
A:Cross-references: GB:M80160
C:Superfamily: neurokinin 1 receptor

Query Match 20.9%; Score 410; DB 2; Length 443;
Best Local Similarity 30.8%; Pred. No. 1.4e-27;
Matches 121; Conservative 68; Mismatches 142; Indels 62; Gaps 13;

Qy 17 GENSKPLGTPYNFSEHCQDSV-----DVMVFIVTSYSTETVGVGLNCLMC 64
Db GPNASSHFVWNYTFSD-WQNFVGRRYGAESQNTVKALLIVAYSFTIVFSGNLVCH 94

Qy 65 VTVRQKEKANVTNLLIANLAFSPFLMCLLCOPLTAVYTIMDYWIFGETLCKMSAFIQMS 124
Db VIFKNQRMHSATSLFVNLAVADIMITLLNTPFTLVFVNSTWVFGKGMCHVSFPAQCS 154

Qy 125 VTVSILSLVALERHQ-----LIINPTGKPSISQAYLGVILW 164
Db LHVSAULTAIVADRHQRPWDFOSLSLHDTLPFPLEVINMHPKPRISITKGVIIYAV 214

Qy 165 VIACVLSPLPLANSILENVFHKHSALEFLADKVVCTESWP-----LAHRTIYTFLL 220
Db VMAFSPSLP---HAICQKLFTEKYSYSDIV-----RSLCLDPFPPADLFWKYLDA 267

Qy 221 FQVCLPLGFLVCYARIYRL-----QRCGRVFKGTYSLAGHMKQNV-VLVVMVAF 276
Db --YLLPLFIISAYARVAKKWLONTIGDVTTEQYLALR--RKKTIVKMLVVLVVF 323

Qy 277 LWPPLHVNLSLEDWHHEAIPICHGNLIFLVCHLLAMASTCVNPFYGFINTNFKKEIK 336
Db CWFPNLCYVLL-----LSSKAHTNNALYPAFWFAMSSCYNPFYICWLNENFRV 379

Qy 337 VLTCCQAPLESEHLP-----LSTVHTEVSKG 364
Db LSWCQR-PPXPQEDRLPSPVSPFVAMTEKSHG 411

RESULT 13
T15622
hypothetical protein C25G6.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Apr-2000
C:Accession: T15622
R:Martin, J.
A:Description: The sequence of C. elegans cosmid C25G6.
A:Reference number: Z18378
A:Accession: T15622
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-455 <MAR>
A:Cross-references: EMBL:U41028; NID:g1086712; PID:g1086716; PIDN:AAA82357.1; CESP:C25G6
A:Gene: CESP:C25G6.5
A:Introns: 37/3; 87/3; 137/2; 203/3; 260/2; 292/3; 346/2; 402/2
C:Superfamily: neurokinin 1 receptor

Query Match 20.1%; Score 395; DB 2; Length 455;
Best Local Similarity 30.8%; Pred. No. 2.9e-26;
Matches 102; Conservative 61; Mismatches 128; Indels 40; Gaps 11;

Qy 25 GTPNFSHCQDSVDVMVFIVTSYSTETVGVGLNCLMCVTVRQKEKANVTNLLIAN 84
Db 30 GTEYSPKE-----FGYFITEATMILFGAIGNFLTIIVILNPMRTTRFFILN 82

Qy 85 FSDPLMCLLCOPLTAVYTIM-DYWIFGETLCKMSAFIQMSVTVSILSLVALERHQ 143

Db 83 LSDFEVCIVTAP-TTLTYLVLMFMPFSRTLCKIAGSLQGFNIFLSTFASIADVRYLI 141

Qy 144 INPTGWPSPISQAYLGVILWVIAVCVLSPLFLANSILENVFHKHSALEFLADKV--VC 201

Db 142 IFPTKRERQNLSCFFIMIWISLILAVELQASDLPVF-----VEPSCDLYAIC 194

Qy 202 ---TESW-PLAHRHTIYTFLLLFQYCLPLGFLIVCYARIYRL-----QRCGRVFKG 251

Db 195 HEQNEIWEKMIISKGTITLAVLITQYAFPLSLVAFYSRIAHRMKLRFANRNQVNTTN 254

Qy 252 TYSIRAG---HMKQNVVLMVVMVAFVLMPL---HVFNSLEDWHHEAIPICHGNLIFL 305

Db 255 TSQRRRSVVERQRTTHLLVCVAVFAVWLPLNVFIHNTFELVNSFSV-----TTF 308

Qy 306 VCHLLAMASTCVNPFYGFINTNFKKEIKAL 336

Db 309 ICHCLAMCSACNPLIYAFNHNRIEFMHL 339

RESULT 14
C40470
glucocorticoid-induced receptor, long form RP82 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 20-Apr-2000
C:Accession: C40470
R:Harrigan, M.T.; Campbell, N.P.; Bourgeois, S.
Mol. Endocrinol. 5, 1331-1338, 1991
A:Title: Identification of a gene induced by glucocorticoids in murine T-cells: a potent
A:Reference number: A40470; MUID:92123228; PMID:1663214
A:Accession: C40470
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-491 <HAR>
A:Cross-references: GB:M80610
C:Superfamily: neurokinin 1 receptor

Query Match 19.7%; Score 387; DB 2; Length 491;
Best Local Similarity 28.1%; Pred. No. 1.5e-25;
Matches 124; Conservative 66; Mismatches 141; Indels 110; Gaps 15;

Qy 17 GENSKPLGTPYNFSEHCQDSV-----DVMVFIVTSYSTETVGVGLNCLMC 64

Db 36 GPNASSHFVWNYTFSD-WQNFVGRRYGAESQNTVKALLIVAYSFTIVFSGNLVCH 94

Qy 65 VTVRQKEKANVTNLLIANLAFSPFLMCLLCOPLTAVYTIMDYWIFGETLCKMSAFIQMS 124

Db 95 VIFKNQRMHSATSLFVNLAVADIMITLLNTPFTLVFVNSTWVFGKGMCHVSFPAQCS 154

Qy 125 VTVSILSLVALERH-----QLIINPTG----- 148

Db 155 LHVSAULTAIVADRHQGLTAIVADRHQGLAQWVPRGDPGGLSPSVTFVLESSLCPA 214

Qy 149 -----W-----KP--SISQAVLGIVLWVIAVCVLSPLFLA 176

Db 215 LFTCKRPMDFOSLSLHDTLPFPLEVINMHPKPRISITKGVIIYAVVWMTFSLP--- 271

Qy 177 NSILENVFHKHSALEFLADKVVCTESWP-----LAHRTIYTFLLLFQYCLPLGFL 232

Db 272 HAICQKLFTEKYSYSDIV-----RSLCLDPFPPADLFWKYLDAFILL--YLLPLFI 325

Qy 233 CYARIYRL-----QRCGRVFKGTYSLAGHMKQNV-VLVVMVAFVLMPLHVFNSLE 288

Db 326 AYARVAKKMLCNTIGDVTTEQYLALR--RKKTIVKMLVVLVVFALCWFPLCYVLL- 382

Qy 289 DWHEAIPICHGNLIFLVCHLLAMASTCVNPFYGFINTNFKKEIKALVITCQOASPLEE 348

Db 383 ---LSSKAHTNNALYPAFWFAMSSCYNPFYICWLNENFRVCLKALLSMCQR-PPK 438

Qy 349 SEHLP-----LSTVHTEVSKG 364

Db 439 EDRLPSPVSPFVAMTEKSHG 459

Search completed: May 11, 2004, 12:57:28
Job time : 23 secs

Search completed: May 11, 2004, 12:57:28
Job time : 23 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2004, 12:50:37 ; Search time 45 Seconds
(without alignments)
2629.318 Million cell updates/sec

Title: US-09-430-775-2

Perfect score: 1965

Sequence: 1 MNTSHLLALLPKSPQGENR.....TVHTEVSKGSLRLSGRSNPI 375

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_arChaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1756	89.4	375	097505	097505 sus scrofa
2	1633.5	83.1	372	11 Q922D4	Q922d4 cavia porce
3	1517	77.2	375	11 Q8BZP9	Q8bzf9 mus musculus
4	1192.5	60.7	377	13 Q8QGM3	Q8qgm3 gallus gall
5	960	48.9	375	13 Q57463	Q57463 brachydanio
6	950.5	48.4	373	13 Q73734	Q73734 brachydanio
7	922	46.9	374	13 Q9YHX1	Q9yhx1 gadus morhu
8	915.5	46.6	377	13 Q73733	Q73733 brachydanio
9	890.5	45.3	365	13 Q8UVW7	Q8uvw7 lampetra fl
10	859.5	43.7	385	13 Q8QFW1	Q8qfm1 gallus gall
11	855.5	43.6	383	6 Q8GK75	Q8gk75 macaca mula
12	573	23.2	290	4 Q98463	Q98463 homo sapien
13	487	24.8	443	13 Q9QFM2	Q9qfm2 gallus gall
14	471	24.0	381	11 Q8BW1	Q8bw1 mus musculus
15	469	23.9	381	11 Q9ERCO	Q9erc0 rattus norv
16	467.5	23.8	446	11 Q925F1	Q925f1 cavia porce

17	467	23.8	600	5	Q9VW75	Q9vw75 drosophila
18	465.5	23.7	445	6	Q9GK73	Q9gk73 macaca mula
19	457.5	23.3	481	5	Q9VNM1	Q9vnm1 drosophila
20	457.5	23.3	485	5	Q8SZ35	Q8sz35 drosophila
21	422.5	21.5	422	11	Q8VHD7	Q8vhd7 rattus norv
22	415	21.1	365	11	Q8BHH0	Q8bhh0 mus musculus
23	403.5	20.5	405	11	Q924N0	Q924n0 mus musculus
24	403	20.5	432	11	Q924G9	Q924g9 rattus norv
25	397	20.2	456	11	Q80T54	Q80t54 mus musculus
26	395	20.1	417	11	Q8BKR6	Q8bkr6 mus musculus
27	394	20.1	417	11	Q924H0	Q924h0 mus musculus
28	393.5	20.0	465	5	O44426	O44426 lymnaea sta
29	392.5	20.0	463	11	Q9EP07	Q9epj7 mus musculus
30	381.5	19.4	457	5	Q18534	Q18534 caenorhabdi
31	378.5	19.3	391	5	Q9GZG8	Q9gzg8 caenorhabdi
32	374	19.0	387	5	Q22188	Q22188 caenorhabdi
33	374	19.0	402	5	Q964E5	Q964e5 dugesia tig
34	374	19.0	430	5	Q810L4	Q810l4 caenorhabdi
35	372	18.9	336	5	Q9Y073	Q9y073 lymnaea sta
36	372	18.9	402	5	Q20275	Q20275 caenorhabdi
37	368.5	18.8	394	5	Q9U721	Q9u721 drosophila
38	368.5	18.8	540	5	Q9VRM0	Q9vrm0 drosophila
39	366	18.6	380	5	Q9NFV0	Q9nfv0 lymnaea sta
40	364	18.5	365	5	Q9XXU4	Q9xxu4 caenorhabdi
41	363	18.5	384	11	Q9QW13	Q9qw13 rattus sp.
42	363	18.5	517	5	Q9VWR3	Q9vwr3 drosophila
43	360	18.3	425	4	Q9HBV6	Q9hbv6 homo sapien
44	359.5	18.3	399	11	Q8K418	Q8k418 rattus norv
45	358	18.2	380	5	Q9NFV3	Q9nfv3 lymnaea sta

ALIGNMENTS

RESULT 1

097505 ID 097505 PRELIMINARY; FRT; 375 AA.
AC Q97505;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Neuropeptide Y receptor type 4 (Neuropeptide Y-family receptor
DE Y4).
GN NPY Y4.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LMD; TISSUE=Kidney;
RA Ito Y., Minezawa M.;
RT "Sus scrofa NPY Y4 gene for neuropeptide Y receptor type 4, complete
RT cds [genomic].";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRED NORWEGIAN LANDRACE;
MEDLINE=20187975; PubMed=10720571;
RA Waith A., Tornsten A., Chardon P., Harbitz I., Chowdhary B.P.,
RA Andersson L., Lundin L.-G., Larhammar D.;
RT "Evolution of the neuropeptide Y receptor family: gene and chromosome
RT duplications deduced from the cloning and mapping of the five receptor
RT subtype genes in the pig.";
RL Genome Res. 10:302-310(2000).
DR EMBL; AF021678; BAA36218.1; -;
DR EMBL; AF227955; AAF62507.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007218; F:neuropeptide signaling pathway; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.

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DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_FL_2; 1.
KW Neuropeptide; Receptor.
SQ SEQUENCE 375 AA; 42346 MW; 5992P075904DBLA0 CRC64;

Query Match      89.4%; Score 1756; DB 6; Length 375;
Best Local Similarity 85.9%; Pred. No. 9.1e-157;
Matches 322; Conservative 29; Mismatches 24; Indels 0; Gaps 0;

QY 1 MNTSHLLALLPKSPQGENRSKPLGTPYNFSEHCQSDVDVMVFIVTSYSETVVGVLGNL 60
DB 1 MNTSHFGLGLFPCAPQGNRSKAKGIPYNFSDHCQSDIDPMVFVVTYSYSETIVGVLGNL 60
QY 61 CLMCVTVRQEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGELCKMSAFI 120
DB 61 CLICVTIRQEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGELCKISAFI 120
QY 121 QCMSVTVSILSLVALERHQLIINPTGKPSISQAYLGIVLWIAVCVLSLPLANSIL 180
DB 121 QCMSVTVSILSLVALERHQLIINPTGKPSVSQAYLGIVLWIAVCVLSLPLANSIL 180
QY 181 ENVFHKHNSKALFLADKVVCTESWPLAHRTIYTTFTLLFOYCLPLGLILVCYARIYR 240
DB 181 QNVFHKHNSKALFLADKVVCTESWPLEHRRIYTTFTLLFOYCIPLAFILVCYRIYOR 240
QY 241 LQGRGVFHKGTVSLRAGHKQNVNVLVAVAFVAVLWPLHVFNSLEDWHHEAIPICHG 300
DB 241 LRKGRGVFHKGAYSSRAQWKMRINGILAAVAVAFVAVLWPLHVFNSLEDWYHEAIPICHG 300
QY 301 NLIFLVCHLLAMASTCNPPIYGFNTNFKKIKALVLTCCQSQAPLESEHPLSTVHTE 360
DB 301 NLIFLVCHLLAMASTCNPPIYGFNTNFKKIKALVLTCCQSQIPVESEHPLSTVQTE 360
QY 361 VSKGSLRLSGRSNPI 375
DB 361 ISKGSRLRLSGRSNPI 375

RESULT 2
Q922D4 PRELIMINARY; PRT; 372 AA.
AC Q922D4;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE Pancreatic polypeptide receptor Y4.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RF MEDLINE=99017377; PubMed=9802391;
RA Eriksson H., Berglund M.M., Holmberg S.K., Kahl U., Gehlert D.R.,
RA Larhammar D.;
RT "The cloned guinea pig pancreatic polypeptide receptor Y4 resembles
RT more the human Y4 than does the rat Y4.";
RL Regul. Pept. 75:29-37(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Sharma P.S., Holmberg S.K., Eriksson H., Beck-Sickinger A.G.,
RA Grundemar L., Larhammar D.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF072822; AAD13144.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1.1;
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.

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DR PROSITE; PS00262; G_PROTEIN_RECEP_FL_2; 1.
KW Receptor.
SQ SEQUENCE 372 AA; 41774 MW; 5B6CF78FBB213374 CRC64;

Query Match      83.1%; Score 1633.5; DB 11; Length 372;
Best Local Similarity 82.9%; Pred. No. 3e-145;
Matches 311; Conservative 22; Mismatches 39; Indels 3; Gaps 1;

QY 1 MNTSHLLALLPKSPQGENRSKPLGTPYNFSEHCQSDVDVMVFIVTSYSETVVGVLGNL 60
DB 1 MDTSPFLASLLPTYPQGENRSKQRLLFNFSDHCQSDGLMGFIVTSYGLETIVGVLGNL 60
QY 61 CLMCVTVRQEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGELCKMSAFI 120
DB 61 CLICVTIRQEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGELCKMSAFI 120
QY 121 QCMSVTVSILSLVALERHQLIINPTGKPSISQAYLGIVLWIAVCVLSLPLANSIL 180
DB 121 QCMSVTVSILSLVALERHQLIINPTGKPSVQAYLGIVLWIAVCVLSLPLANSIL 180
QY 181 ENVFHKHNSKALFLADKVVCTESWPLAHRTIYTTFTLLFOYCLPLGLILVCYARIYR 240
DB 181 ENVFHKHNSKALFLADKVKACKESWPLGHRVYVYTTFTLLFOYCIPLAFILVCYLRISWR 240
QY 241 LQGRGVFHKGTVSLRAGHKQNVNVLVAVAFVAVLWPLHVFNSLEDWHHEAIPICHG 300
DB 241 LRQGRGVLC---SSRAGQMKRINGVLVAVGAPVAVLWPLHVFNSLEDWHHEAIPYCHG 297
QY 301 NLIFLVCHLLAMASTCNPPIYGFNTNFKKIKALVLTCCQSQAPLESEHPLSTVHTE 360
DB 298 NLIFLVCHLLAMASTCNPPIYGFNTNFKKIKALVLTCCQSLPPSESEHPLSTLHTE 357
QY 361 VSKGSLRLSGRSNPI 375
DB 358 VSKGFLPLGGRSNPI 372

RESULT 3
Q8BZF9 PRELIMINARY; PRT; 375 AA.
AC Q8BZF9;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Neuropeptide Y receptor type 4.
GN PPYRI.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Urinary bladder;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK035505; SACC29082.1; -.
DR MGD; MGI:105374; Ppyr1.
DR GO; GO:0001602; F:pancreatic polypeptide receptor activity; IEA.
DR GO; GO:0001601; F:peptide yy receptor activity; IEA.
DR InterPro; IPR000362; Fumarate lyase.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1.1;
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00163; FUMARATE LYASES; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_FL_2; 1.
SQ SEQUENCE 375 AA; 42657 MW; 638EBA110E7F7A53 CRC64;

Query Match      77.2%; Score 1517; DB 11; Length 375;

```

Best Local Similarity 75.6%; Pred. No. 2.7e-134; Indels 0; Gaps 0;
Matches 282; Conservative 35; Mismatches 56;

QY 1 MNTSHLLALLPKSPQGENRSGPLGTPYNFSEHQDSDVDMVFIVTSYSIETVGVGLGNL 60

Db 1 MNTSHFLAPLFFGSLQGNNGTNPLDSDPYNFSGQDQDGAELAFITTYSTETLGVGLGNL 60

QY 61 CLMCVTVROKSKANVTNLLIANLAFSLFMCCLLQPLTAVYTYNDYWFVGETLCKNSAFI 120

Db 61 CLIFVTRQKESNVNLLIANLAFSLFMCCLLQPLTAVYTYNDYWFVGETLCKMTFI 120

QY 121 QCMSTVTSILSVLVALERHQLIINPTGKPSISQAYLGIIVLWIAVCLSLPLFLANSIL 180

Db 121 QCMSTVTSILSVLVALERHQLIINPTGKPSISQAYLGIIVWVFCFLSLPLFLANSTL 180

QY 181 ENVTHQNSKALEFLADKVCWCTESWPLAHRITITTELLLFQYCLPGLFVLCVARIYR 240

Db 181 NDLFHYNSKVEELEDKVCWCFVSWSSDHRHLITITTELLLFQYCIPLAFVLCVARIYR 240

QY 241 LQRCGRVPHKGTYSURAGHMKQNVVLVWVAVAVLWPLHVNLSLEDWHEAIPICHG 300

Db 241 LQRCGRVPHKGTYSURAGHMKQNVVLVWVAVAVLWPLHVNLSLEDWHEAIPICHG 300

QY 301 NLIFLVCHLLAMASTCVNPPFYGLINTNPKKEIKALVTCQOSAPLSEHPLSTVHTE 360

Db 301 NLIFLVCHLLAMASTCVNPPFYGLINTNPKKEIKALVTCQOSAPLSEHPLSTVHTE 360

QY 361 VSKGSLRLSGRSN 373

Db 361 LSKGSMRMGSKSN 373

RESULT 4

Q8QGM3 PRELIMINARY; PRT; 377 AA.
ID Q8QGM3
AC Q8QGM3
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Neuropeptide Y receptor 4.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;

RP SEQUENCE FROM N.A.
RA Lundell I., Boswell T., Larhammar D.;
RT "Chicken Neuropeptide Y Family Receptor Y4; a Receptor with Equal
RT Affinity for Pancreatic Polypeptide, Neuropeptide Y and Peptide YY."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF140853; AAL84161.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein-coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_FL_2; 1.
KW Receptor.

QY SEQUENCE 377 AA; 42972 NW; C9EC6C00DBFD1F9E CRC64;
Query Match 60.7%; Score 1192.5; DB 13; Length 377;
Best Local Similarity 60.4%; Pred. No. 8.9e-104; Indels 3; Gaps 1;
Matches 218; Conservative 60; Mismatches 80;

QY 18 ENRSKFLGTPYNFSEHQDSDVDMVFIVTSYSIETVGVGLGNLCLMCVTVROKSKANVTN 77

Db 17 KNLNSRSPFSLNQCRNVTDLTFLATYSLETVLGVGVNGLICLVIAVROKSKANVTN 76

QY 78 LLIANLAFSDFLMCLLQPLTAVYTYNDYWFVGETLCKNSAFIQCMSTVTSILSVLVAL 137

Db 77 ILISNLIISDLFMCVCLPFTVYTYNDYWFVGEWCKMTSTQCTSTVTSILSVLVAL 136

QY 138 ERHQLIINPTGKPSISQAYLGIIVLWIAVCLSLPLFLANSILENVFHHKSKALEFLAD 197

Db 137 ERHQLIINPTGKPSISQAYLGIIVLWIAVCLSLPLFLANSILENVFHHKSKALEFLAD 196

QY 198 KVCCTESWPLAHRITITTELLLFQYCLPGLFVLCVARIYERLQRCGRVPHKGTYSUR 257

Db 197 KAICIDSWPSEORHLIITTELLLFQYCLPGLFVLCVARIYERLQRCGRVPHKGTYSUR 256

QY 258 GNMKQNVVLVWVAVAVLWPLHVNLSLEDWHEAIPICHGNIIFLVCHLLAMASTCV 317

Db 257 VQLRRINIULASVAAFAVCMPLHVNITVDWYVKIISPCHHNLIFSLCHLVAMASTCV 316

QY 318 NFPIYGLINTNPKKEIKALVTCQO---SAPLESEHPLSTVHTEVSKGSLRLSGRSNP 374

Db 317 NPVIYGLFNSNPKKEIKALVTCQO---SAPLESEHPLSTVHTEVSKGSLRLSGRSNP 374

QY 375 I 375

Db 377 I 377

RESULT 5

O57463 PRELIMINARY; PRT; 375 AA.
ID O57463
AC O57463
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Neuropeptide Y /peptide YY receptor Yb.
GN NPYRYB.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;

RN [1]
RP SEQUENCE FROM N.A.
RA Lundell I., Berglund M.M., Starback P., Salaneck S., Gehlert D.R.,
RA Larhammar D.;
RT "Cloning and characterization of a novel neuropeptide Y (NPY) receptor
RT subtype in the zebrafish."
RL DNA Cell Biol. 0:0-0(1997).
DR EMBL; AF030245; AAB94616.1; -.
DR ZFIN; ZDB-GENE-980526-208; npyryb.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein-coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_FL_2; 1.
KW Receptor.

QY SEQUENCE 375 AA; 42116 MW; 4B0C9551131A14D1 CRC64;
Query Match 48.9%; Score 960; DB 13; Length 375;
Best Local Similarity 50.1%; Pred. No. 6.5e-82;
Matches 188; Conservative 57; Mismatches 112; Indels 18; Gaps 3;

QY 1 MNTSHLLALLPKSPQGENRSGPLGTPYNFSEHQDSDVDMVFIVTSYSIETVGVGLGNL 60

Db 1 MERSHL-----NNSSWLEDP-----TCPASLSTFLIYAVSTMLAVGVNT 44

QY 61 CLMCVTVROKSKANVTNLLIANLAFSDFLMCLLQPLTAVYTYNDYWFVGETLCKNSAFI 120

Db 45 CLVAVITROKEMENVTNIFIVNLSCSDILVCLVLEVTIITLMDRWILGEALCKVTPFV 104

QY 121 QCMSTVTSILSVLVALERHQLIINPTGKPSISQAYLGIIVLWIAVCLSLPLFLANSIL 180

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Db      105 QCMSTVTSIFSMVLIALERHQLIHPGTMKPVVRHSYLA VAVIWIACISIFLPSFNIL 164
Qy      181 ENVFHKHKSALBFLADKVVCTESWPLAHRITTTTFLLLFOYCLPLGFLVCYARIYR 240
Db      165 TNSPFHNLSPFPNPFSDHFCICQWSEGNELTYTTLLLCQCLPLALLVCYFRIFLR 224
Qy      241 LQGRGRVH--KGTYSURAGHMKQNVVLMVAVFVAVLMLPLHVPNSLEDWHHEAIPIC 298
Db      225 LSRKQDVERARGORQKAKGSRKRVNAMLASIVAFAALCWLPLNVENTIFFDNWHEAIPVC 284
Qy      299 HGNLPLVCHLLAMASTCVNPFYVGLNTNFKKEIKALVLTCCOASAPLESEHPLSTVH 358
Db      285 QHDAIFSACHLTAMASTCVNPFYVGLNNTNFQELKSLSCRCWCPAESYZSFFLSTVS 344
Qy      359 TEVSKGSLRLSGRSN 373
Db      345 TGITKGSILNGSGAS 359

RESULT 6
ID O73734 PRELIMINARY; PRT; 373 AA.
AC O73734;
DT 01-AUG-1998 (TReMBLrel. 07, Created)
DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Neuropeptide Y/peptide YY receptor Yc.
GN NPYRYC OR NPYRYC.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96068842; PubMed=9407007;
RA Lundell I., Berglund M.M., Starback P., Salaneck E., Gehlert D.R.,
RA Latham D.;
RT "Cloning and characterization of a novel neuropeptide Y receptor
RT subtype in the zebrafish."
RL DNA Cell Biol. 16:1357-1363 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96068393; PubMed=9434780;
RA Ringvall M., Berglund M.M., Larhammar D.;
RT "Multiplicity of neuropeptide Y receptors: cloning of a third distinct
RT subtype in the zebrafish."
RL Biochem. Biophys. Res. Commun. 241:749-755 (1997).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF037401; AAC41277.1; -.
DR ZFIN; ZDB-GENE-990415-175; npyryc.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL2_1; 1.
DR KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 373 AA; 41673 MW; 217DA7F51A940CFD CRC64;

Query Match 48.4%; Score 950.5; DB 13; Length 373;
Best Local Similarity 53.6%; Pred. No. 5e-81;
Matches 181; Conservative 60; Mismatches 94; Indels 3; Gaps 2;

Qy      31 SEHQDSVDVMVFVTSYSIETVGVGLNCLMCVTVRQEKANVTNLLIANLAFSDFLM 90
Db      20 SNVCEPSVSGTLLIVASTVIAVGLVNTCLVFIISRQEMRVNVTNLLIANLSCSDILM 79
Qy      91 CLLCQPLTAVTMDYTFGSLCKMSAFIOMSVTVSILSLVALERHQLINPTGWK 150

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Db      80 CWCPLPTVIITLMDRWILGETLCKVTFPQCMSTVTSIFSLVIALERHQLIHPGTWT 139
Qy      151 PSISOAYLGIIVIAVIAVLSLPLANSILENVFHKHKSALBFLADKVVCTESWPLAHH 210
Db      140 PAAGSHYLA VAVTWMVACFSLPFLSNILTNAPFQNIPLFPNPSDHVICMELWPSERN 199
Qy      211 RTIYTFLLFOYCLPLGFLVCYARIYRRLQGRGVFHKGTYS--LRAGHMKQNVVLY 268
Db      200 RLAVTTSLLFOYCLPLGFLVCYARIYRRLQGRGVFHKGTYS--LRAGHMKQNVVLY 259
Qy      269 VMVAVFVAVLPLHVPNSLEDWHHEAIPICGNLFLVCHLLAMASTCVNPFYVGLNTN 328
Db      260 VIVAFALCWLPLNVENTIFFDNWHEAIPACQHDVIFSACHLTAMASTCVNPFVVGFLNTN 319
Qy      329 FKKEIKALVLTCCOASAPLEES-EHLPLSTVHTEVSKGS 365
Db      320 FQKELKATLQRCNCGWGVPEYTFESFPLSTVATDYSKVS 357

RESULT 7
QYHX1
ID QYHX1 PRELIMINARY; PRT; 374 AA.
AC QYHX1;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Neuropeptide Y/peptide YY receptor Yb.
GN NPYRB.
OS Gadus morhua (Atlantic cod).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
OC NCBI_TaxID=8049;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99017378; PubMed=9802392;
RA Arvidsson A.K., Wraith A., Jonsson-Rylander A.C., Larhammar D.;
RT "Cloning of a neuropeptide Y/peptide YY receptor from the Atlantic
RT cod: the Yb receptor."
RL Regul. Pept. 75:39-43 (1998).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF073925; AAD2833.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL2_1; 1.
DR KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 374 AA; 42260 MW; D2A9C9516C4998E2 CRC64;

Query Match 46.9%; Score 922; DB 13; Length 374;
Best Local Similarity 51.3%; Pred. No. 2.4e-78;
Matches 178; Conservative 62; Mismatches 95; Indels 12; Gaps 4;

Qy      32 EHCQDSVDVMVFVTSYSIETVGVGLNCLMCVTVRQEKANVTNLLIANLAFSDFLMC 91
Db      28 EBCPSKSGTTFLLVYSTMTIAGVIGNSCLFVIARQKEMHVNVTNFIANLSCSDILMC 87
Qy      92 LLCQPLTAVTMDYTFGSLCKMSAFIOMSVTVSILSLVALERHQLINPTGWKP 151
Db      88 IFCLPVTLLIYTMDSRWILGEALCKLTPFVQCISVTSVTSIFSLVIANERYQLIHPGTWKP 147
Qy      152 SISOAYLGIIVIAVIAVLSLPLANSILENVFHKHKSALBFLA-DKVCTESWPLAHH 210
Db      148 MVGQSYMAVGIIVVAVCLISVPSFSLFTVLDNLPLQNLS--LPFPQDHWLCTESWPTNSN 205
Qy      211 RIYTFLLFOYCLPLGFLVCYARIYRRLQGRGVFHKGTYSLRAGHK---QNVTVL 267

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Db 206 RLAVTSSLLVFOYFLPLGLIAACVLSIFLRURRRKDMVERARDSSRNRRAKSSRRINWML 265
QY 268 VMVAVAFVAVLPLHVFNSLEDHHEALPICHGNLILFLVCHLLAVASTCVNPFYGLFNT 327
Db 266 GSVIALFAVCVPLNFINFTVDFWHELMVSCOHNLIFSVCVHLVAVASTCVNPFVYGLFNS 325
QY 328 NFKKEIKALVLTCCQSAAPLESSEHLPLSTVATEV-----SKGSRL 368
Db 326 NFKQKATLHCRWGAARVYENPLSAVSTEVTKESHMSKGSISI 372

RESULT 8
ID 073733 PRELIMINARY; PRT; 377 AA.
AC 073733;
DT 01-AUG-1998 (TRENBLrel. 07, Created)
DT 01-AUG-1998 (TRENBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Neuroptide Y/peptide Y receptor ya.
GN NPVRYA OR NPVRYA.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=98068942; PubMed=9407007;
RA Lundell I., Berglund M.M., Starback P., Salaneck E., Gehlert D.R.,
RA Larhammar D.;
RT "Cloning and characterization of a novel neuroptide Y receptor
RT subtype in the zebrafish";
RL DNA Cell Biol. 16:1357-1363(1997).
RN [2]
SEQUENCE FROM N.A.
RP MEDLINE=9806333; PubMed=9434780;
RA Ringvall M., Berglund M.M., Larhammar D.;
RA "Multiplicty of neuroptide Y receptors: cloning of a third distinct
RT subtype in the zebrafish";
RL Biochem. Biophys. Res. Commun. 241:749-755(1997).
RN [3]
SEQUENCE FROM N.A.
RP MEDLINE=99337783;
RA Starback P., Lundell I., Fredriksson R., Berglund M.M., Van Y.L.,
RA Wraith A., Soderberg C., Postlethwait J.H., Larhammar D.;
RA "Neuroptide Y receptor subtype with unique properties cloned in the
RT zebrafish: the zra receptor";
RL Brain Res. Mol. Brain Res. 70:242-252(1999).
DR EMBL; AF037400; AAC41276.1; -.
DR HSSP; P02699; 1F88.
DR ZFIN; ZDB-GENE-980526-393; npvrya.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 377 AA; 42901 MW; 60562AD9C7BF5D0 CRC64;

Query Match 46.6%; Score 915.5; DB 13; Length 377;
Best Local Similarity 49.1%; Pred. No. 1e-77;
Matches 172; Conservative 70; Mismatches 89; Indels 19; Gaps 5;

QY 34 CQDSVDVMVFIVTSYISTVGVGLNCLMCMVTVRQKEKANVTNLLIAFSDFLMCLL 93
Db 35 CQMSPTMTLLVLCVLLGLNLLIICIMHDPDPNVTIILIANLSVDILSVF 94
QY 94 CQPLTAVTMDYWFGETLCKNSAFIQCMSTVTSILSLVALERHQLIINPTGWKPSI 153
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Db 95 CLPFTVYVTLMDHWIFGALLCRIMPFCQSVTSVLSLVLIATERHQLILHPSGKPSV 154
QY 154 SQAYGLIVLIWVIACVLSLPFLANSILENVFKHNSKALEP-----LADKVVCTESWPLAH 209
Db 155 PQAYIAVLVFWLLACVTSLPFLA-----PHLLTSEPYSLFPAPLSQOVCLVMPQSOD 207
QY 210 HRTIYTTFLLLFQYCLPLGLFIIVCYARIYRRLQQRVF-----HKGTYSLRAGHKQV 263
Db 208 HKLAYTTSLLFQYCCPLLMLLCYLIFLRLQRRERMLERQCSRNRDEHRRVHMSKEI 267
QY 264 NVVLVNVVAFVAVLPLHVFNSLEDHHEALPICHGNLILFLVCHLLAVASTCVNPFYIG 323
Db 268 NVMLATLVAAFAVCVPLNFAVADCDQEVLPVCNHLFLSLCHLLAMSSTCVNPFYIG 327
QY 324 FLNTNFKKEIKALVLTCCQSAAPLESSEHLPLSTVHTEVSKGSLRLSGRS 372
Db 328 FLNSNFKKDVASVVLHC-HFQPLEDSYEHFPMSTMWTDVSRISFRLRNS 376

RESULT 9
QY 08UVW7 PRELIMINARY; PRT; 365 AA.
AC 08UVW7;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE NPY receptor.
OS Lampetra fluviatilis (River lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Lampetra.
OC NCBI_TaxID=7748;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=21590343; PubMed=11733009;
RA Salaneck E., Fredriksson R., Larson E.T., Conlon J.M., Larhammar D.;
RT "A neuroptide Y receptor Y1-subfamily gene from an agnathan, the
RT European river lamprey. A potential ancestral gene.";
RL Eur. J. Biochem. 268:6146-6154(2001).
CC -I- SUBCELLULAR LOCATION. INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF340022; AAL66410.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 365 AA; 41060 MW; 9EB5FD3BB5607E9 CRC64;

Query Match 45.3%; Score 890.5; DB 13; Length 365;
Best Local Similarity 48.3%; Pred. No. 2.2e-75;
Matches 172; Conservative 67; Mismatches 106; Indels 11; Gaps 2;

QY 29 NFSE-----HCQDSVDVMVFIVTSYISTVGVGLNCLMCMVTVRQKEKANVTNLLIA 81
Db 8 NWSEMPQLDLDHQQTQAVRSFVIATYCVLIAGLGLNSLLVLIIRHSELHNTNIIIV 67
QY 82 NLAFSDFLMCLICQPLTAVTMDYWFGETLCKNSAFIQCMSTVTSILSLVALERHQL 141
Db 68 NLAFSDFLMCLVGLVCLPTIATYIATYIATYIATYIATYIATYIATYIATYIATYI 127
QY 142 LIINPTGWKPSISQAYGLIVLIWVIACVLSLPFLANSILENVFKHNSKALEFLADKVV 201
Db 128 LIINPTGWKPSLNHVAICATWAAFAKSSFLAFHVLTDPEYRNLSHFYDYGEKVC 187
QY 202 TESWPLAHRTYTTTFLLFQYCLPLGLFIIVCYARIYRRLQQRVF-----HKGTYSLR 257
Db 188 IEVVALGHLKFAFTTSLLVFQFSCPLLFLVCLYIFLRLQRRKMLPTGREGGNGVRA 247
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QY 258 GHMKQNVVVLVAVAVLWFLVHVNLSLEWHHEAIPICGNLIPLVCHLLAVASTCV 317
DB 248 SHMKINMLVAIVAGFAICWLPYTFNAVDWNPITLLHCHQDLIFSLCHLTAMLSICI 307

QY 318 NPFIYGLNTNFKEIKALVLTCCQAPLEESHLPLSTVHTVSKGSLRLSGSN 373
DB 308 NPFIYGLNNFLKELKATILRCQCPVEEDFENFLSTWNTDISKGSURFSCKNS 363

RESULT 10
Q8QPM1 PRELIMINARY; PRT; 385 AA.
ID Q8QPM1
AC Q8QPM1; 2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Neuropeptide Y receptor Y1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22060921; PubMed=12065655;
RA Holmberg S.K.S.; Mikko S.; Boswell T.; Zoorob R.; Larhammar D.;
RT "Pharmacological characterization of cloned chicken neuropeptide Y
RT receptors Y1 and Y5."
RL J. Neurochem. 81:462-471(2002).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AY040845; AAK83557.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 385 AA; 44365 MW; DEAA905C89D3A584 CRC64;

Query Match 43.7%; Score 859.5; DB 13; Length 385;
Best Local Similarity 44.5%; Pred. No. 1.9e-72;
Matches 173; Conservative 74; Mismatches 111; Indels 31; Gaps 7;

QY 1 MNTSHLLALLPKSPOGENRSKPLGTPYNS-----EHCDSVDVMVFIIVTSYS 49
DB 1 MNASVL-----DPLGNNSH-----LNFSEKNSQILOFEDDCHVPLAMFTLALAG 48

QY 50 IETVVGVLGNLCMVTVROKENVNLLIANLAFSDFMLCCLCOPLTAVTYIMDYWIF 109
DB 49 TVIILGVSGNLALIVILKQKENVNLLIYNLSFSDLLVMTIMCLPFTFVYTLMDHWIF 108

QY 110 GETLCKMSAFIOCMSTVLSLVALERHOLIINPTGWKPSISOAYLGIWLIWIACV 169
DB 109 GEAWCKLNPNVQCASTVSVLSLVAIERHOLIINPRGWRPNRRHAYGIAAWLWATA 168

QY 170 LSLPFLANSILENVFHNKHSKALEFLADKVVCTESWPLAHHRTIYTTFLLLFOYCLPLGF 229
DB 169 SSLPFLIYHVLTDPPFNIT--PDEYKDKYVCLDLPLDPLDARLSYTTLLIIVQYFGPLCF 226

QY 230 ILVCYARIYELQROGEVFKGYIS--LRAGHKQNVNVLVAVAVLWFLVHVNLSLE 288
DB 227 IFICYLKIYPLRLKSNMMDKRSYSRSETKRINIMLSIVAVAVCWLPFTIIVIF 286

QY 289 DWHEALPI--CHGNLIPLVCHLLAVASTCVNPFYGLNTNFKEIKALVLTCCQASPL 346
DB 287 DWNHEILPVATCSHNLFLIHLTAMISTCVNPFYGLNKNFORDLQFLPFHCHFSRSE 346
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QY 347 BESHLPLSTVHTVSKGSLRLSGRSNPI 375
DB 347 EDETAMSTMTDVSRTSLK--QASPV 372

RESULT 11
Q9GK75 PRELIMINARY; PRT; 383 AA.
ID Q9GK75
AC Q9GK75;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Neuropeptide Y receptor Y1.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21184974; PubMed=11287088;
RA Gehlert D.R.; Yang P.; George C.; Wang Y.; Schober D.;
RA Gackenhimer S.; Johnson D.; Beavers L.S.; Gadski R.A.; Baez M.;
RT "Cloning and characterization of Rhesus monkey neuropeptide Y receptor
RT subtypes (1).";
RL Peptides 22:343-350(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF303089; AAG40771.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 383 AA; 44306 MW; F872C45AA90DF62A CRC64;

Query Match 43.6%; Score 856.5; DB 6; Length 383;
Best Local Similarity 44.6%; Pred. No. 3.6e-72;
Matches 166; Conservative 77; Mismatches 108; Indels 21; Gaps 5;

QY 16 QGENRSKPLGTPYNSF-----HCQDSVDVMVFIIVTSYSIETVVGVLGNLCMC 64
DB 8 QVENHS-----VHSNFSEKNAQLAFENDCHLPLAMIFTLALAYGAVIILGVSGNLALII 63

QY 65 VTVCKEKANVTNLLIANLAFSDFMLCCLCOPLTAVTYIMDYWIFGETLCKMSAFIOCMS 124
DB 64 IILKQKENVNLLIYNLSFSDLLVMTIMCLPFTFVYTLMDHWVFGAMCKLNFFVOCVS 123

QY 125 VTVSILSLVALERHOLIINPTGWKPSISOAYLGIWLIWIACVLSLPLANSILENVF 184
DB 124 ITVSIFSLVLIATERHOLIINPRGWRPNRRHAYGIAWLVAVASSLPELIYQVMTDEP 183

QY 185 HKHNSKALEFLADKVVCTESWPLAHHRTIYTTLLFOYCLPLGFLVCYARIYRR--ORQ 244
DB 184 FQN--VTLDAYDKYVCFDPPSDSHLSLTLLLLVQYFGPLCFIFICFKIYIRURR 241

QY 245 GRVFHK--GTYSLRAGHKQNVNVLVAVAVLWFLVHVNLSLEWHHEAIPICGNLI 303
DB 242 NNMWDMKRNKYRSRSETKRINIMLSIVAVAVCWLPFTIIVTVDWNHQLIATCNELL 301

QY 304 FLVCHLLAMASTCVNPFYGLNTNFKEIKALVLTCCQAPLEESHLPLSTVHTVSK 363
DB 302 FLCHLTAMISTCVNPFYGLNKNFORDLQFFNFCDFRSRDDDDYETIAMSTMTDVS 361

QY 364 GSLRLSGRSNPI 375
DB 362 TSLK--QASPV 370
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RESULT 12
Q99463 ID Q99463 PRELIMINARY; PRT; 290 AA.
AC Q99463;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE y6 encoding protein.
OS y6.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97066888; PubMed=8910290;
RA Matsunoto M., Nomura T., Momose K., Ikeda Y., Kondou Y., Akiho H.,
RA Togami J., Kimura Y., Okada M., Yamaguchi T.;
RT "Inactivation of a novel neuropeptide Y/peptide YY receptor gene in
RT primate species.";
RL J. Biol. Chem. 271:27217-27220(1996).
DR EMBL; D86519; BAA13103.1; -.
DR Genbank; HGNC:7959; NPY6R.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0004983; F:neuropeptide Y receptor activity; TAS.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR SEQUENCE 290 AA; 33180 MW; 3ECCD587001CA8DB CRC64;

Query Match 29.2%; Score 573; DB 4; Length 290;
Best Local Similarity 40.5%; Pred. No. 1.2e-45;
Matches 106; Conservative 65; Mismatches 89; Indels 2; Gaps 2;

QY 21 SKPLGTPNFSEHQDSVDVMVFVTSYSIETVGVGLNCLMCVTYRQKEKA-NVTNLL 79
D 15 TKNNSAFFYFESCPPSPALLLCIAVTVLIVGLFGLNLSIIIFKKQKKAQNFSTIL 74
QY 80 IANLAFSDFLMCLLCOPTAVTYTMDYIFGETLCKMSAFIQCMSTVTSILSLVLVALER 139
D 75 IANLSLSDTLVCMGCIHFTIITLMDHIFGDTWCRLTSYVQSVSISVIFSLFTAVR 134
QY 140 HOLINPTGWKPSISQAYLGVLIWVIAVLSPFLANSILENVFKNHKSALFLADKV 199
D 135 YQLIVNPRGWKPSYTHAWGITLWLPSSLISIPFLSYHLTDFPNNLSLPTDLYTHQV 194
QY 200 VCTESWPLAHRHTYTTTFLLLFOYCLPLGVLCVARIYRLOQ-GRVFKGTYSLRAG 258
D 195 ACVENWPSKDRLLPTTSLFLQYFVPLGFLICVLCIRRNKAVDKKKEGRLN 254
QY 259 HMKQNVNVLVWVAVAVLWLP 280
D 255 ENKRINTWLSIVTFGACWLP 276

RESULT 13
Q8QFM2 ID Q8QFM2 PRELIMINARY; PRT; 443 AA.
AC Q8QFM2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Neuropeptide Y receptor Y5.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=22060921; PubMed=12065655;
RA Holmberg S.K.S., Mikko S., Boswell T., Zoorob R., Larhammar D.;
RT "Pharmacological characterization of cloned chicken neuropeptide Y
RT receptors Y1 and Y5.";
RL J. Neurochem. 81:462-471(2002).
DR EMBL; AY040844; AAK93556.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR SEQUENCE 443 AA; 50044 MW; EFE9F1A391CC092E CRC64;

Query Match 24.8%; Score 487; DB 13; Length 443;
Best Local Similarity 26.7%; Pred. No. 2.3e-37;
Matches 115; Conservative 69; Mismatches 124; Indels 122; Gaps 9;

QY 26 TPNFS--EHCQDSV-DVMVFVTSYSIETVGVGLNCLMCVTYRQKEKANVTNLLIAN 82
D 20 TTKNFSAMEDYKSSVDDIQYFLIGHYTLISLAGFVGNLLVLTALTKRKQK-TIINILGN 78
QY 83 LAFSDFLMCLLCOPTAVTYTMDYIFGETLCKMSAFIQCMSTVTSILSLVLVALERHOL 142
D 79 LAFSDILVVLFCSPFTLSVLLDRWFGVVMCHINFPFLOCTSVLSTLMLISIAAVRYEM 138
QY 143 IINPTGWKPSISQAYLGVLIWVIAVLSPFLANSILENVFHK-----NHSKALEFLADK 198
D 139 VKYPLSSNLTAKHGYFLIIVWAVGCAICSP-----PVFHKIVDLHKLTLNLEALNR 191
QY 199 VCTESWPLAHRHTYTTTFLLLFOYCLPLGVLCVARIYR-----RLQGRGVFHK--- 250
D 192 LUCISWPSDSVRIAPTISLLLMQVILPLVCLTASHTSVCRSVGSLSSKEGKFOENEM 251
QY 251 -----GTYSIRAGH-----MKQNVN-----LVWV 271
D 252 NULHPSKSAQTEAQPSSHTSWSCALVRKHRRYSKKTSTVMPAILRQODADFDRLPET 311
QY 267 -----LVWV 271
D 312 SGTEKSQSSSKFPGVPCFEMKPEENTEQDMITVSQSIIRKTRRRVFCRLTVLI 371
QY 272 VAFAVLWLPFLHFNLSLEDWHHEAIPICHGNIILFLVCHLLAMASTCVNPFYIYGLNTNFKK 331
D 372 LVFGSWMPLHLFHVITDENATLISNRHFKLVYCYICHLIGMWSCLNPLIYGLFNNSIKA 431
QY 332 EYKALVLTQ 341
D 432 DLMSLIPCCQ 441

RESULT 14
Q8BWV1 ID Q8BWV1 PRELIMINARY; PRT; 381 AA.
AC Q8BWV1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Neuropeptide Y receptor type 2.
GN NPY2R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Hippocampus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
```

RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR ENBL; AK049892; BAC33975.1; -.
DR MGD; MGI:108418; Npy2.
DR GO: GO:0001601; F:peptide YY receptor activity; IDA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR InterPro; IPR001220; LECTIN_legB.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G PROTEIN RECEPT_F1_1; 1.
DR PROSITE; PS00262; G PROTEIN RECEPT_F1_2; 1.
DR PROSITE; PS00307; LECTIN_LEGME_BETA; 1.
DR PROSITE; PS00307; LECTIN_LEGME_BETA; 1.
DR GO: GO:0001601; F:peptide YY receptor activity; IDA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR InterPro; IPR001220; LECTIN_legB.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G PROTEIN RECEPT_F1_1; 1.
DR PROSITE; PS00262; G PROTEIN RECEPT_F1_2; 1.
DR PROSITE; PS00307; LECTIN_LEGME_BETA; 1.
DR PROSITE; PS00307; LECTIN_LEGME_BETA; 1.
SQ SEQUENCE 381 AA; 42628 MW; 30787C051347884A CRC64;

Query Match 24.0%; Score 471; DB 11; Length 381;
Best Local Similarity 32.5%; Pred. No. 6.4e-36;
Matches 122; Conservative 67; Mismatches 148; Indels 38; Gaps 10;

QY 15 PQGENRSKPLG-TPYNPSEHCQDS---VDVMVFIVTSYSIETVGVGLNLCMCVTVRQK 70
DB 20 PYGCHTTPRGEPLPDPEPELIDSTKLVEVQVLLAYCSIIILGVGNSLVHVVIKF 79
QY 71 EKANVTNLLIANAFSDFLMCLLCQPLTAVITMDYWFGETLCKMSAFIQCMSTVTSIL 130
DB 80 SMRTVTNFFIANLAVADLLVNTLCPLPTLTITLMGEWKGVPVLCVLAQGLAVQVSTI 139
QY 131 SLVLVALERHQLINPTGPKPSISOAYLGVLVIAVCLSLP---FLANSILENVFHN 187
DB 140 TLTVTALDRHCIVVHLESKISKQISFLIIGLANGVSALLASPLAFREYSLEI 195
QY 188 HSKALEFLADKVVCTESWP---LAHRTIYTTFTLLFOYCLPLGFTILVCVARIYRLQ 244
DB 196 ----PDF---EIVACTEKWPGEKSVYGVTSLLIYVLPGLIISFSYTRIWSKLNH 249
QY 245 GRVPHKGTYSIRAGHKQVNVLMVAVFVAVLWLPVHVSNSLEDWHEHAIPCHGNLIF 304
DB 250 VSPGAASDHYHQRH--KMTKMLVCVVVFAVSWLPVLAQVLDVDSHVDLKEVKLIF 307
QY 305 LVCHLLAVASTCVNPFYIGFANTNFKKEIKALVLTCCQSAAPLESEHPLSTVHTVEVS-- 362
DB 308 TVFHIIAMCSTFANPLLYGWNNSYRKAFLS-APRCQR-----LDATSEVSMVT 356
QY 363 ---KGSRLSGRNSP 374
DB 357 FKAKKNLEVKKNKGP 371

RESULT 15
Q9ERC0 PRELIMINARY; PRT; 381 AA.
AC Q9ERC0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Neuropeptide Y/peptide YY-Y2 receptor.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Small intestine;
RA Voisin T., Goumain M., LaBurthe M.;
RT "Cloning of a cDNA encoding a rat type 2 neuropeptide Y/peptide YY
receptor expressed in intestinal epithelial crypt cells."
RL Submitted (JUL-2000) to the ENBL/GenBank/DBSJ databases.
DR ENBL; AY004257; AAF89094.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsin.

DR InterPro; IPR001220; LECTIN_legB.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G PROTEIN RECEPT_F1_1; 1.
DR PROSITE; PS00262; G PROTEIN RECEPT_F1_2; 1.
DR PROSITE; PS00307; LECTIN_LEGME_BETA; 1.
DR PROSITE; PS00307; LECTIN_LEGME_BETA; 1.
KW Receptor.
SQ SEQUENCE 381 AA; 42510 MW; 659327904B288BC7 CRC64;

Query Match 23.9%; Score 469; DB 11; Length 381;
Best Local Similarity 32.4%; Pred. No. 9.8e-36;
Matches 125; Conservative 63; Mismatches 132; Indels 66; Gaps 12;

QY 12 PKSPQGENRSKPLGTPYNPSEHCQDS---VDVMVFIVTSYSIETVGVGLNLCMCVTVR 68
DB 25 PTTTRGE-----LPPDPEPELIDSTKLVEVQVLLAYCSIIILGVGNSLVHVVIK 77
QY 69 QKEKANTNLLIANAFSDFLMCLLCQPLTAVITMDYWFGETLCKMSAFIQCMSTVTS 128
DB 78 FKSMTVTNFFIANLAVADLLVNTLCPLPTLTITLMGEWKGVPVLCVLAQGLAVQVS 137
QY 129 ILSVLVALERHQLINPTGPKPSISOAYLGVLVIAVCLSLP---FLANSILENVFHN 185
DB 138 TITVTALDRHCIVVHLESKISKQISFLIIGLANGVSALLASPLAFREYSLEI 195
QY 186 KHSKALEFLADKVVCTESWP---LAHRTIYTTFTLLFOYCLPLGFTILVCVARIYRLQ 242
DB 196 ----PDF---EIVACTEKWPGEKSVYGVTSLLIYVLPGLIISFSYTRIWSKLNK 247
QY 243 ----RGRVPHKGTYSIRAGHKQVNVLMVAVFVAVLWLPVHVSNSLEDW 290
DB 248 NHVSPGAASDHYHQRH--KMTKMLVCVVVFAVSWLPVLAQVLDVDSHVDLKEVKL 293
QY 291 RHEAIPCHGNLIFLVCHLLAVASTCVNPFYIGFANTNFKKEIKALVLTCCQSAAPLESE 350
DB 294 DSHVLDLKEVKLIETVFIHAMCSTFANPLLYGWNNSYRKAFLS-APRCQR----- 345
QY 351 HLPSTVHTVEVS---KGSRLSGRNS 373
DB 346 ---LDATSEVSMVTFKAKKNLEVKKN 368

Search completed: May 11, 2004, 12:56:56
Job time : 48 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2004, 12:50:37 ; Search time 23 Seconds
(without alignments)
841.728 Million cell updates/sec

Title: US-09-430-775-2

Perfect score: 1965
Sequence: 1 MNTSHLLALLPKSPQGNR.....TVHTEVSKGSLRSGRSNPI 375

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
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3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCFUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	1965	100.0	375	1 US-08-176-412-2	Sequence 2, Appli
2	1965	100.0	375	2 US-08-555-268A-2	Sequence 2, Appli
3	1965	100.0	375	2 US-08-495-695B-2	Sequence 2, Appli
4	1965	100.0	375	4 US-09-200-673-17	Sequence 17, Appli
5	1965	100.0	375	5 PCT-US94-14436-2	Sequence 2, Appli
6	1839	93.6	350	2 US-08-495-695B-33	Sequence 33, Appli
7	1492	75.9	375	2 US-08-495-695B-28	Sequence 28, Appli
8	1492	75.9	375	5 PCT-US94-14436-28	Sequence 28, Appli
9	1412	71.9	350	2 US-08-495-695B-32	Sequence 32, Appli
10	869	44.2	382	2 US-08-555-268A-13	Sequence 13, Appli
11	867	44.1	382	2 US-08-415-818-7	Sequence 7, Appli
12	867	44.1	382	2 US-08-894-236-7	Sequence 14, Appli
13	867	44.1	382	5 PCT-US96-01444-7	Sequence 14, Appli
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15	863	43.9	371	1 US-08-415-818-6	Sequence 6, Appli
16	863	43.9	371	2 US-08-894-236-6	Sequence 6, Appli
17	863	43.9	371	2 US-08-919-624-4	Sequence 4, Appli
18	863	43.9	371	5 PCT-US96-01444-6	Sequence 6, Appli
19	860.5	43.8	384	4 US-09-200-673-15	Sequence 15, Appli
20	856.5	43.6	383	3 US-09-045-186-2	Sequence 2, Appli
21	856.5	43.6	384	1 US-08-233-144-4	Sequence 4, Appli
22	856.5	43.6	384	2 US-08-555-268A-15	Sequence 15, Appli
23	856.5	43.6	384	4 US-10-013-846-4	Sequence 4, Appli
24	856.5	43.6	384	5 PCT-US93-05039-3	Sequence 3, Appli
25	854.5	43.5	411	3 US-08-817-869-3	Sequence 3, Appli
26	854.5	43.5	411	5 PCT-US95-14377-3	Sequence 3, Appli
27	823.5	41.9	370	1 US-08-415-818-12	Sequence 12, Appli

28 823.5 41.9 370 2 US-08-894-236-12 Sequence 12, Appli
29 823.5 41.9 370 5 PCT-US96-01444-12 Sequence 12, Appli
30 705.5 35.9 301 1 US-08-118-270-72 Sequence 72, Appli
31 705.5 35.9 301 5 PCT-US93-08528-72 Sequence 72, Appli
32 618.5 31.5 228 3 US-08-513-974B-313 Sequence 313, App
33 618.5 31.5 228 3 US-08-513-974B-362 Sequence 362, App
34 618.5 31.5 228 3 US-08-776-971-130 Sequence 130, App
35 556.5 28.3 394 4 US-10-013-846-17 Sequence 17, Appli
36 487.5 24.8 370 3 US-09-172-353-2 Sequence 2, Appli
37 487.5 24.8 370 3 US-09-172-353-3 Sequence 3, Appli
38 487.5 24.8 370 4 US-09-799-955-2 Sequence 2, Appli
39 487.5 24.8 370 4 US-09-799-955-3 Sequence 3, Appli
40 485.5 24.7 370 3 US-08-513-974B-26 Sequence 26, Appli
41 485.5 24.7 370 3 US-08-513-974B-323 Sequence 323, App
42 485.5 24.7 370 3 US-09-172-353-5 Sequence 5, Appli
43 485.5 24.7 370 3 US-08-776-971-21 Sequence 21, Appli
44 485.5 24.7 370 3 US-08-776-971-104 Sequence 104, App
45 485.5 24.7 370 4 US-09-799-955-5 Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-08-176-412-2
; Sequence 2, Application US/08176412
; Patent No. 5516653
; GENERAL INFORMATION:
; APPLICANT: Bard, Jonathan A.
; APPLICANT: Walker, Mary
; APPLICANT: Branchek, Theresa
; APPLICANT: Weinshank, Richard L.
; TITLE OF INVENTION: DNA ENCODING A HUMAN NEUROPEPTIDE
; TITLE OF INVENTION: Y/PEPTIDE VY/PANCREATIC POLYPEPTIDE
; TITLE OF INVENTION: RECEPTOR (Y4) AND USES THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/176,412
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44743/JPW/TEP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-176-412-2

Query Match 100.0%; Score 1965; DB 1; Length 375;
Best local Similarity 100.0%; Pred No. 5, 2e-144;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNTSHLLALLPKSPQGNRSLPTGPNFSEHCQSDVDMVFIYTSYIETVGVGLNL 60

Db 1 MNTSHLLALLPKSPQGENSKPLGTPYNFSEHCQSDVDWVFIWTSYSIETVGVGLNL 60
QY 61 CLMCVTVROKEXANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFI 120
Db 61 CLMCVTVROKEXANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFI 120
QY 121 QCMSTVTSIISLVVALERHQLIINPTGKWPISQAYLGIWLIWIAVLSLPLANSIL 180
Db 121 QCMSTVTSIISLVVALERHQLIINPTGKWPISQAYLGIWLIWIAVLSLPLANSIL 180
QY 181 ENVFHKNHSALEFLADKVVCTESWPLAHRTIYTTFFLLFOYCLPLGFIIVCYARIYR 240
Db 181 ENVFHKNHSALEFLADKVVCTESWPLAHRTIYTTFFLLFOYCLPLGFIIVCYARIYR 240
QY 241 LQRCGRVFKGTYSLRAGHKQNVVAVAFVWLVPLHVFNSLEDWHEAIPICHG 300
Db 241 LQRCGRVFKGTYSLRAGHKQNVVAVAFVWLVPLHVFNSLEDWHEAIPICHG 300
QY 301 NLIFLVCHLLAMASTCVNPFYGFNTNFKKEIKALVLTCCQSAPLESEHPLSTVHTE 360
Db 301 NLIFLVCHLLAMASTCVNPFYGFNTNFKKEIKALVLTCCQSAPLESEHPLSTVHTE 360
QY 361 VSKGSLRSLGRSNPI 375
Db 361 VSKGSLRSLGRSNPI 375

RESULT 2
US-08-555-268A-2
; Sequence 2, Application US/08555268A
; Patent No. 5958709
; GENERAL INFORMATION:
; APPLICANT: Bard, Jonathan A.
; APPLICANT: Walker, Mary
; APPLICANT: Branchek, Theresa
; APPLICANT: Weinshank, Richard L.
; TITLE OF INVENTION: DNA ENCODING A HUMAN NEUROPEPTIDE
; TITLE OF INVENTION: Y/PEPTIDE YY/PANCREATIC POLYPEPTIDE
; TITLE OF INVENTION: RECEPTOR (Y4) AND USES THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,268A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44743-Z/JPW/MAT
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0526
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-555-268A-2
Query Match 100.0%; Score 1965; DB 2; Length 375;

Best Local Similarity 100.0%; Pred. No. 5.2e-144;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNTSHLLALLPKSPQGENSKPLGTPYNFSEHCQSDVDWVFIWTSYSIETVGVGLNL 60
Db 1 MNTSHLLALLPKSPQGENSKPLGTPYNFSEHCQSDVDWVFIWTSYSIETVGVGLNL 60
QY 61 CLMCVTVROKEXANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFI 120
Db 61 CLMCVTVROKEXANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFI 120
QY 121 QCMSTVTSIISLVVALERHQLIINPTGKWPISQAYLGIWLIWIAVLSLPLANSIL 180
Db 121 QCMSTVTSIISLVVALERHQLIINPTGKWPISQAYLGIWLIWIAVLSLPLANSIL 180
QY 181 ENVFHKNHSALEFLADKVVCTESWPLAHRTIYTTFFLLFOYCLPLGFIIVCYARIYR 240
Db 181 ENVFHKNHSALEFLADKVVCTESWPLAHRTIYTTFFLLFOYCLPLGFIIVCYARIYR 240
QY 241 LQRCGRVFKGTYSLRAGHKQNVVAVAFVWLVPLHVFNSLEDWHEAIPICHG 300
Db 241 LQRCGRVFKGTYSLRAGHKQNVVAVAFVWLVPLHVFNSLEDWHEAIPICHG 300
QY 301 NLIFLVCHLLAMASTCVNPFYGFNTNFKKEIKALVLTCCQSAPLESEHPLSTVHTE 360
Db 301 NLIFLVCHLLAMASTCVNPFYGFNTNFKKEIKALVLTCCQSAPLESEHPLSTVHTE 360
QY 361 VSKGSLRSLGRSNPI 375
Db 361 VSKGSLRSLGRSNPI 375

RESULT 3
US-08-495-695B-2
; Sequence 2, Application US/08495695B
; Patent No. 5976814
; GENERAL INFORMATION:
; APPLICANT: Bard, Jonathan A.
; APPLICANT: Walker, Mary
; APPLICANT: Branchek, Theresa
; APPLICANT: Weinshank, Richard L.
; TITLE OF INVENTION: DNA ENCODING A HUMAN NEUROPEPTIDE
; TITLE OF INVENTION: Y/PEPTIDE YY/PANCREATIC POLYPEPTIDE
; TITLE OF INVENTION: RECEPTOR (Y4) AND USES THEREOF
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/495,695B
; FILING DATE: 13-Jan-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44743-A-PCT-US/JPW/JHB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-495-695B-2

Query Match 100.0%; Score 1965; DB 2; Length 375;
Best Local Similarity 100.0%; Pred. No. 5.2e-144;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNTSHLLALLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYIETVGVGLNL 60
DB 1 MNTSHLLALLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYIETVGVGLNL 60

QY 61 CLMCVTVRQKEKANTNLLIANLAFSDFLMCLLCOPLTAVTMDYWFGETLCKMSAFI 120
DB 61 CLMCVTVRQKEKANTNLLIANLAFSDFLMCLLCOPLTAVTMDYWFGETLCKMSAFI 120

QY 121 QCMSTVTSILSVLVALERHQIINPTGKPKSISQAYLGIVLIWVIACVLSLPLFANSIL 180
DB 121 QCMSTVTSILSVLVALERHQIINPTGKPKSISQAYLGIVLIWVIACVLSLPLFANSIL 180

QY 181 ENVFHNKHSKALEFLADKVVCTESPLAHRITITFTLLFOYCLPLGFIIVCYARIYR 240
DB 181 ENVFHNKHSKALEFLADKVVCTESPLAHRITITFTLLFOYCLPLGFIIVCYARIYR 240

QY 241 LORQGRVFKGTYSIRAGHKQNVVLYVMVAVAVLWPLHVFNSLEDWHHEAIPICHG 300
DB 241 LORQGRVFKGTYSIRAGHKQNVVLYVMVAVAVLWPLHVFNSLEDWHHEAIPICHG 300

QY 301 NLIFLVCHLLAMASTCWNPFYGFINTNFKKEIKALVLTCCQSAPLESEHPLSTVHTE 360
DB 301 NLIFLVCHLLAMASTCWNPFYGFINTNFKKEIKALVLTCCQSAPLESEHPLSTVHTE 360

QY 361 VSKGSLRLSGRSNPI 375
DB 361 VSKGSLRLSGRSNPI 375

RESULT 4
US-09-200-673-17
; Sequence 17, Application US/09200673A
; Patent No. 6316203
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe P.G.
; APPLICANT: Weinschank, Richard L.
; APPLICANT: Walker, Mary W.
; APPLICANT: Branchek, Theresa
; TITLE OF INVENTION: Methods of Modifying Feeding Behavior, Compounds Useful
; TITLE OF INVENTION: in Such Methods, and DNA Encoding A Hypothalamic
; TITLE OF INVENTION: Atypical Neuropeptide Y/Peptide Y Receptor (Y5)
; FILE REFERENCE: 46166-BZ/JPW
; CURRENT APPLICATION NUMBER: US/09/200,673A
; CURRENT FILING DATE: 1998-11-25
; EARLIER APPLICATION NUMBER: 08/566,096
; EARLIER FILING DATE: 1995-12-01
; EARLIER APPLICATION NUMBER: 08/349,025
; EARLIER FILING DATE: 1994-12-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 17
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-200-673-17

Query Match 100.0%; Score 1965; DB 4; Length 375;
Best Local Similarity 100.0%; Pred. No. 5.2e-144;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNTSHLLALLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYIETVGVGLNL 60
DB 1 MNTSHLLALLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYIETVGVGLNL 60

QY 61 CLMCVTVRQKEKANTNLLIANLAFSDFLMCLLCOPLTAVTMDYWFGETLCKMSAFI 120
DB 61 CLMCVTVRQKEKANTNLLIANLAFSDFLMCLLCOPLTAVTMDYWFGETLCKMSAFI 120

QY 121 QCMSTVTSILSVLVALERHQIINPTGKPKSISQAYLGIVLIWVIACVLSLPLFANSIL 180
DB 121 QCMSTVTSILSVLVALERHQIINPTGKPKSISQAYLGIVLIWVIACVLSLPLFANSIL 180

QY 181 ENVFHNKHSKALEFLADKVVCTESPLAHRITITFTLLFOYCLPLGFIIVCYARIYR 240
DB 181 ENVFHNKHSKALEFLADKVVCTESPLAHRITITFTLLFOYCLPLGFIIVCYARIYR 240

QY 241 LORQGRVFKGTYSIRAGHKQNVVLYVMVAVAVLWPLHVFNSLEDWHHEAIPICHG 300
DB 241 LORQGRVFKGTYSIRAGHKQNVVLYVMVAVAVLWPLHVFNSLEDWHHEAIPICHG 300

QY 301 NLIFLVCHLLAMASTCWNPFYGFINTNFKKEIKALVLTCCQSAPLESEHPLSTVHTE 360
DB 301 NLIFLVCHLLAMASTCWNPFYGFINTNFKKEIKALVLTCCQSAPLESEHPLSTVHTE 360

QY 361 VSKGSLRLSGRSNPI 375
DB 361 VSKGSLRLSGRSNPI 375

RESULT 5
PCT-US94-14436-2
; Sequence 2, Application PC/TUS9414436
; GENERAL INFORMATION:
; APPLICANT: Bard, Jonathan A.
; APPLICANT: Walker, Mary
; APPLICANT: Branchek, Theresa
; APPLICANT: Weinschank, Richard L.
; TITLE OF INVENTION: DNA ENCODING A HUMAN NEUROPEPTIDE
; TITLE OF INVENTION: Y/PEPTIDE YY/PANCREATIC POLYPEPTIDE
; TITLE OF INVENTION: RECEPTOR (Y4) AND USES THEREOF
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/14436
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44743-A-PCT\JPW\MAT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-14436-2

Query Match 100.0%; Score 1965; DB 5; Length 375;
Best Local Similarity 100.0%; Pred. No. 5.2e-144;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNTSHLLALLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYIETVGVGLNL 60
DB 1 MNTSHLLALLPKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYIETVGVGLNL 60

Query Match 75.9%; Score 1492; DB 2; Length 375;
Best Local Similarity 75.1%; Pred. NO. 1.4e-107;
Matches 280; Conservative 34; Mismatches 59; Indels 0; Gaps 0

QY 1 MNTSHLLALLPKSPQGENRSKPLGTYPNFSHCQSDVDMVVFIVTSYSETVVGVLGNL 60
Db 1 MNTSHLLALLPKSPQGENRSKPLGTYPNFSHCQSDVDMVVFIVTSYSETVVGVLGNL 60
QY 61 CLMCVTVROKQKANTVLLIANLAFSDFLMCLLCOPLTAVYTIMDYWIFGETLCKMSAFI 120
Db 61 CLMCVTVROKQKANTVLLIANLAFSDFLMCLLCOPLTAVYTIMDYWIFGETLCKMSAFI 120
QY 121 QCMSTVTSILSLVALERHQLIINPTGKWPISQAYLGIWLVIAVLSLPLFLANSIL 180
Db 121 QCMSTVTSILSLVALERHQLIINPTGKWPISQAYLGIWLVIAVLSLPLFLANSIL 180
QY 181 ENVFHKNHSALEFLADKVCVTSWPLAHRTIYTTFFLLFYQCLPLGLFVLCVARIYRR 240
Db 181 ENVFHKNHSALEFLADKVCVTSWPLAHRTIYTTFFLLFYQCLPLGLFVLCVARIYRR 240
QY 241 LORQGRVTHKGTYSURAGHKQVNVVAVFAVLWLPVFNLSLDDWHHEALPICHG 300
Db 241 LORQGRVTHKGTYSURAGHKQVNVVAVFAVLWLPVFNLSLDDWHHEALPICHG 300
QY 301 NLIFLVCHLLAMASTCVNPFTYGFINTNFKEIKALVLTQCOQSAFLSEHPLSTVHTE 360
Db 301 NLIFLVCHLLAMASTCVNPFTYGFINTNFKEIKALVLTQCOQSAFLSEHPLSTVHTE 360
QY 361 VSKGSLRLSGRSN 373
Db 361 LSKGSMRMGSKSN 373

RESULT 8

PCT-US94-14436-28
; Sequence 28, Application PC/TUS9414436
; GENERAL INFORMATION:
; APPLICANT: Bard, Jonathan A.
; APPLICANT: Walker, Mary
; APPLICANT: Branchek, Theresa
; APPLICANT: Weinshank, Richard L.
; TITLE OF INVENTION: DNA ENCODING A HUMAN NEUROPEPTIDE
; TITLE OF INVENTION: Y/PEPTIDE YV/PANCREATIC POLYPEPTIDE
; TITLE OF INVENTION: RECEPTOR (Y4) AND USES THEREOF
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/14436
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44743-A-PCT\JPW\MAT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-14436-28

Query Match 75.9%; Score 1492; DB 5; Length 375;
Best Local Similarity 75.1%; Pred. No. 1.4e-107;
Matches 280; Conservative 34; Mismatches 59; Indels 0; Gaps 0;
QY 1 MNTSHLLALLPKSPQGENRSKPLGTYPNFSHCQSDVDMVVFIVTSYSETVVGVLGNL 60
Db 1 MNTSHLLALLPKSPQGENRSKPLGTYPNFSHCQSDVDMVVFIVTSYSETVVGVLGNL 60
QY 61 CLMCVTVROKQKANTVLLIANLAFSDFLMCLLCOPLTAVYTIMDYWIFGETLCKMSAFI 120
Db 61 CLMCVTVROKQKANTVLLIANLAFSDFLMCLLCOPLTAVYTIMDYWIFGETLCKMSAFI 120
QY 121 QCMSTVTSILSLVALERHQLIINPTGKWPISQAYLGIWLVIAVLSLPLFLANSIL 180
Db 121 QCMSTVTSILSLVALERHQLIINPTGKWPISQAYLGIWLVIAVLSLPLFLANSIL 180
QY 181 ENVFHKNHSALEFLADKVCVTSWPLAHRTIYTTFFLLFYQCLPLGLFVLCVARIYRR 240
Db 181 ENVFHKNHSALEFLADKVCVTSWPLAHRTIYTTFFLLFYQCLPLGLFVLCVARIYRR 240
QY 241 LORQGRVTHKGTYSURAGHKQVNVVAVFAVLWLPVFNLSLDDWHHEALPICHG 300
Db 241 LORQGRVTHKGTYSURAGHKQVNVVAVFAVLWLPVFNLSLDDWHHEALPICHG 300
QY 301 NLIFLVCHLLAMASTCVNPFTYGFINTNFKEIKALVLTQCOQSAFLSEHPLSTVHTE 360
Db 301 NLIFLVCHLLAMASTCVNPFTYGFINTNFKEIKALVLTQCOQSAFLSEHPLSTVHTE 360
QY 361 VSKGSLRLSGRSN 373
Db 361 LSKGSMRMGSKSN 373

RESULT 9

US-08-495-695B-32
; Sequence 32, Application US/08495695B
; Patent No. 5976814
; GENERAL INFORMATION:
; APPLICANT: Bard, Jonathan A.
; APPLICANT: Walker, Mary
; APPLICANT: Branchek, Theresa
; APPLICANT: Weinshank, Richard L.
; TITLE OF INVENTION: DNA ENCODING A HUMAN NEUROPEPTIDE
; TITLE OF INVENTION: Y/PEPTIDE YV/PANCREATIC POLYPEPTIDE
; TITLE OF INVENTION: RECEPTOR (Y4) AND USES THEREOF
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/495,695B
; FILING DATE: 13-Jan-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44743-A-PCT-US/JPW/JHB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-495-695B-32

Query Match 71.9%; Score 1412; DB 2; Length 350;
Best Local Similarity 75.7%; Pred. No. 1.9e-101;
Matches 265; Conservative 30; Mismatches 55; Indels 0; Gaps 0;

QY 1 MNTSHLLALLPKSPGKNSKPLGTPYNFSEHCDSVDVWVPIVTSYSIETVVGVLGNL 60
DB 1 MNTSHLLASLSPAFLOGKNGTNPDLNLSQCDQSDADLLAFITTTYSVEVLGVLGNL 60
QY 61 CLMCVTVROKESKANVTNLLIANLAFSDFLMCLLCQPLTAVTYIMDYWIFGETLCKOSAPI 120
DB 61 CLIFVITROKESKANVTNLLIANLAFSDFLMCLLCQPLTAVTYIMDYWIFGEVLCKMLAFI 120
QY 121 QCMVTVTSLSVLVLEHQLIINTGWKPSISQAYLGIWLVIAVLSLPLANSIL 180
DB 121 QCMVTVTSLSVLVLEHQLIINTGWKPSISQAYLGIWLVIAVLSLPLANSIL 180
QY 181 ENVFHKNHSALEFLADKVVCTESWPLAHRHTIYTTFFLLFQYCLPLGLFVLCYARIYR 240
DB 181 NDLFHNHSAKVFELEDKVVCFVSWSDHRLIYTTFFLLFQYCLPLGLFVLCYARIYR 240
QY 241 LQQRVFKHTYSLRAGHMKQNVVWVAFVAVLWPLVFNLSLEDDHHEAIPICHG 300
DB 241 LQQRFAFHTHTCSSRVGQMKRNGMLAMVTAFAVLWPLVFNLTLEDWYQEAIPACHG 300
QY 301 NLIFLCHLLAMASTCVNPIYGLTNFKKEIKALVLTQQSAPLESEE 350
DB 301 NLIFLCHLFAMASTCVNPIYGLTNFKKEIKALVLTQQSAPLESEE 350

RESULT 10

US-08-555-268A-13
; Sequence 13, Application US/08555268A
; Patent No. 5958709

GENERAL INFORMATION:

APPLICANT: Bard, Jonathan A.
APPLICANT: Walker, Mary
APPLICANT: Branchek, Theresa
APPLICANT: Weinshank, Richard L.
TITLE OF INVENTION: DNA ENCODING A HUMAN NEUROPEPTIDE
TITLE OF INVENTION: V/PEPTIDE XY/PANCREATIC POLYPEPTIDE
TITLE OF INVENTION: RECEPTOR (Y4) AND USES THEREOF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/555,268A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 44743-Z/JWP/MAT
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 382 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-555-268A-13

Query Match 44.2%; Score 869; DB 2; Length 382;
Best Local Similarity 46.8%; Pred. No. 1.4e-59;
Matches 168; Conservative 74; Mismatches 101; Indels 16; Gaps 4;

QY 28 YNFESEH-----CQDSVDVWVPIVTSYSIETVVGVLNCLMCVTVROKESKANVTN 77
DB 16 YNVSNEPFLAFENDCHLPLAVIFTLAAYGAVIILGVSGLNLAIIILIKQEMRNVTN 75
QY 78 LLIANLAFSDFLMCLLCQPLTAVTYIMDYWIFGETLCKOSAPIQCMVTVTSLSVLVAL 137
DB 76 ILIIVLSFSDLLVAVMCLPFTFVTVLMDHWFGETWCKLMPFVQCVSITVIFSLVLIIV 135
QY 138 ERHQLIINTGWKPSISQAYLGIWLVIAVLSLPLANSILNVFNHSHKALEFLAD 197
DB 136 ERHQLIINTGWKPSISQAYLGIWLVIAVLSLPLANSILNVFNHSHKALEFLAD 193
QY 198 KVVCTESWPLAHRHTIYTTFFLLFQYCLPLGLFVLCYARIYRLOQRVFKHTYS-LR 256
DB 194 KYVCFDKEPDSHRLSYTTLLLVLYQFGLCFICVFKIYIRLGRNMMWDKIRDSKYR 253
QY 257 AGHMKQNVVWVAFVAVLWPLVFNLSLEDDHHEAIPICHGNLIFLCHLLAMASTC 316
DB 254 SSETKRINVMLLSIWAFVAVLWPLTIFNTVFDNHHQIIATCNHNLFLFLCHLTAMISTC 313
QY 317 VNPIYGLTNFKKEIKALVLTQQSAPLESEEHLPLSTVHTVSVKSGSLRSGRSNPI 375
DB 314 VNPIYGLTNFKKEIKALVLTQQSAPLESEEHLPLSTVHTVSVKSGSLRSGRSNPI 375

RESULT 11

US-08-415-818-7
; Sequence 7, Application US/08415818
; Patent No. 5621079

GENERAL INFORMATION:

APPLICANT: Cascieri, Margaret A.
APPLICANT: Linemeyer, David L.
APPLICANT: MacNeil, Douglas J.
APPLICANT: Shiao, Lin-Lin
APPLICANT: Strader, Catherine D.
APPLICANT: Tan, Carina P.
APPLICANT: Weinberg, David H.
TITLE OF INVENTION: NEUROPEPTIDE Y RECEPTOR
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mary A. Appollina
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/415,818
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/383,746
FILING DATE: 03-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Appollina, Mary A.
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19390
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3462

TELEFAX: 908-594-4720
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 382 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-415-818-7

Query Match 44.1%; Score 867; DB 1; Length 382;
Best Local Similarity 46.5%; Pred. No. 2e-59;
Matches 167; Conservative 75; Mismatches 101; Indels 16; Gaps 4;

QY 28 YNFSER-----CQDSVDVMVPIVTSYISITVWGLNCLMCVTVRQKEMNVTN 77
DB 16 YNASESPLLAFENDCHPLAVIFTLALAYGAVILGVSGNLALIIILKQKEMNVTN 75

QY 78 LLIANLAFSDFLMCLLCOPLTAVTMDYWFGETLCKMSAFIQCMSTVLSLVLVAL 137
DB 76 ILIVNLSFSDLLVAVMCLPFTFYTLMDHWVFGETMCKLNPVQCVSITVSIFSLVLI 135

QY 138 ERHQLIINPTGKPSISOAYLGIVLIWVIACVLSLPLFLANSILENVFHNKHSKALEFLAD 197
DB 136 ERHQLIINPRGWRPNRRHAYIGITVWLAVASSLPFVIYQILTDEPQNVS--LAAPKD 193

QY 198 KVCYTESWPLAHRITTYTFFLLFOYCLPLGFIIVCVARIYRRLQQRGVPHKGTYS-LR 256
DB 194 KYVCFDKFSDSHRLSYTLLVLQYFGPLCFIFICYFYIYRLKRNMMDKIRDSKYR 253

QY 257 AGHKQVNVVLVVMVAVAVLWPLHVFNSLEDWHEAIPICHGNLILFVCHLLAMASTC 316
DB 254 SSETKRINIMLSIVAVAVCMPLTIFNTVFDNHNQIATCNHNLFLCHLTAMISTC 313

QY 317 VNPFTYGFINTNFKKEIKALVLTCCQASAPLESEHPLSTVHTEVSKSLSRSGNPI 375
DB 314 VNPFIYGFINKNFQDLQFFNFCDFRSRDDDYETIAMSTVHTDVKTSLSK--QASPV 369

RESULT 12
US-08-894-236-7
; Sequence 7, Application US/08894236
; Patent No. 5939263
; GENERAL INFORMATION:
; APPLICANT: Cascieri, Margaret A.
; APPLICANT: Lineneyer, David L.
; APPLICANT: MacNeil, Douglas J.
; APPLICANT: Shiao, Lin-Lin
; APPLICANT: Strader, Catherine D.
; APPLICANT: Tan, Carina P.
; APPLICANT: Weinberg, David H.
; TITLE OF INVENTION: NEUROPEPTIDE Y RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mary A. Appollina
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/894,236
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/383,746

FILING DATE: 03-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/415,818
; FILING DATE: 03-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Appollina, Mary A.
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19390Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-594-3462
; TELEFAX: 908-594-4720
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 382 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-894-236-7

Query Match 44.1%; Score 867; DB 2; Length 382;
Best Local Similarity 46.5%; Pred. No. 2e-59;
Matches 167; Conservative 75; Mismatches 101; Indels 16; Gaps 4;

QY 28 YNFSER-----CQDSVDVMVPIVTSYISITVWGLNCLMCVTVRQKEMNVTN 77
DB 16 YNASESPLLAFENDCHPLAVIFTLALAYGAVILGVSGNLALIIILKQKEMNVTN 75

QY 78 LLIANLAFSDFLMCLLCOPLTAVTMDYWFGETLCKMSAFIQCMSTVLSLVLVAL 137
DB 76 ILIVNLSFSDLLVAVMCLPFTFYTLMDHWVFGETMCKLNPVQCVSITVSIFSLVLI 135

QY 138 ERHQLIINPTGKPSISOAYLGIVLIWVIACVLSLPLFLANSILENVFHNKHSKALEFLAD 197
DB 136 ERHQLIINPRGWRPNRRHAYIGITVWLAVASSLPFVIYQILTDEPQNVS--LAAPKD 193

QY 198 KVCYTESWPLAHRITTYTFFLLFOYCLPLGFIIVCVARIYRRLQQRGVPHKGTYS-LR 256
DB 194 KYVCFDKFSDSHRLSYTLLVLQYFGPLCFIFICYFYIYRLKRNMMDKIRDSKYR 253

QY 257 AGHKQVNVVLVVMVAVAVLWPLHVFNSLEDWHEAIPICHGNLILFVCHLLAMASTC 316
DB 254 SSETKRINIMLSIVAVAVCMPLTIFNTVFDNHNQIATCNHNLFLCHLTAMISTC 313

QY 317 VNPFTYGFINTNFKKEIKALVLTCCQASAPLESEHPLSTVHTEVSKSLSRSGNPI 375
DB 314 VNPFIYGFINKNFQDLQFFNFCDFRSRDDDYETIAMSTVHTDVKTSLSK--QASPV 369

RESULT 13
US-08-555-268A-14
; Sequence 14, Application US/08555268A
; Patent No. 5958709
; GENERAL INFORMATION:
; APPLICANT: Bard, Jonathan A.
; APPLICANT: Walker, Mary
; APPLICANT: Branchek, Theresa
; APPLICANT: Weinshank, Richard L.
; TITLE OF INVENTION: DNA ENCODING A HUMAN NEUROPEPTIDE
; TITLE OF INVENTION: Y/PEPTIDE YY/PANCREATIC POLYPEPTIDE
; TITLE OF INVENTION: RECEPTOR (Y4) AND USES THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/555,268A
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 44743-2/JPW/MAT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 278-0400
 TELEFAX: (212) 391-0526
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 382 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-555-268A-14

Query Match 44.1%; Score 867; DB 2; Length 382;

Best Local Similarity 46.5%; Pred. No. 2e-59;
 Matches 167; Conservative 75; Mismatches 101; Indels 16; Gaps 4;

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QY 28 YNFSEH-----CQDSVDVMVFIVTSYETVGVGLNCLMCVTVROKQKAVTN 77
Db 16 YNASENSPLAFENDDCHLPLAVFTLAYAGVILGVSGNLALIIILKQKERNVTN 75

QY 78 LLIANLAFSFLMCLCOPLTAVYTIMDYWIFGETLCKMSAFIQCMVTVSILSLVLVAL 137
Db 76 ILIVNLSFSDLLVAVMCLPFTFVYTLMDHWVFGTCKLNPFFVQCVSITVSIFSLVLIIV 135

QY 138 ERHQLINPTGKPSISQAVLGVLINVIACVLSLPLANSILENVFHKHNSKALEFLAD 197
Db 136 ERHQLINPRGWRNNRHAYIGITVWLVAVASLFPVIQILTDFFQNVS--LAAPKD 193

QY 198 KVCVTESWPLAHRHTIYTTFLLLFYQCLPLGFIIVCYVARIYRLQGRVFHKGTYS-LR 256
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QY 257 AGHKQVNVVLVWVAVAFVWLPVHVNLSLEDDHHEAIPICHGNLIFLVCHLLAMASTC 316
Db 254 SSETKRINIMLLSVVAFVAVCWPLTIFNTVFDNNHQIATCNENLFLCHLTAMISTC 313

QY 317 VNPFIYGLNTNFKKEIKALVLTCCQSAPLESEHPLSTVHTVEVSKGSLRSGRSNPI 375
Db 314 VNPFIYGLNKNFORDLQFFNFCDFRSRDDDYETIAMSTMHTDVSKTSLK---QASPV 369

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RESULT 14
 PCT-US96-01444-7

Sequence 7, Application PC/TUS9601444
 GENERAL INFORMATION:
 APPLICANT: Cascieri, Margaret A.
 APPLICANT: Linemeyer, David L.
 APPLICANT: MacNeil, Douglas J.
 APPLICANT: Shiao, Lin-Lin
 APPLICANT: Strader, Catherine D.
 APPLICANT: Tan, Carina P.
 APPLICANT: Weinberg, David H.
 TITLE OF INVENTION: NEUROPEPTIDE Y RECEPTOR
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Mary A. Appollina
 STREET: P.O. Box 2000, 126 E. Lincoln Ave.
 CITY: Rahway
 STATE: NJ
 COUNTRY: USA
 ZIP: 07065
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/01444
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/383,746
 FILING DATE: 03-FEB-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/415,818
 FILING DATE: 03-APR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Appollina, Mary A.
 REGISTRATION NUMBER: 34,087
 REFERENCE/DOCKET NUMBER: 19390Y
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 908-594-3462
 TELEFAX: 908-594-4720
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 382 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 PCT-US96-01444-7

Query Match 44.1%; Score 867; DB 5; Length 382;

Best Local Similarity 46.5%; Pred. No. 2e-59;
 Matches 167; Conservative 75; Mismatches 101; Indels 16; Gaps 4;

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QY 28 YNFSEH-----CQDSVDVMVFIVTSYETVGVGLNCLMCVTVROKQKAVTN 77
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QY 78 LLIANLAFSFLMCLCOPLTAVYTIMDYWIFGETLCKMSAFIQCMVTVSILSLVLVAL 137
Db 76 ILIVNLSFSDLLVAVMCLPFTFVYTLMDHWVFGTCKLNPFFVQCVSITVSIFSLVLIIV 135

QY 138 ERHQLINPTGKPSISQAVLGVLINVIACVLSLPLANSILENVFHKHNSKALEFLAD 197
Db 136 ERHQLINPRGWRNNRHAYIGITVWLVAVASLFPVIQILTDFFQNVS--LAAPKD 193

QY 198 KVCVTESWPLAHRHTIYTTFLLLFYQCLPLGFIIVCYVARIYRLQGRVFHKGTYS-LR 256
Db 194 KYVCFDPPSDSHRLSYTTLLLVQYFGPLCFIFICYFKIYIRLKRNNMMDKIRDSKYR 253

QY 257 AGHKQVNVVLVWVAVAFVWLPVHVNLSLEDDHHEAIPICHGNLIFLVCHLLAMASTC 316
Db 254 SSETKRINIMLLSVVAFVAVCWPLTIFNTVFDNNHQIATCNENLFLCHLTAMISTC 313

QY 317 VNPFIYGLNTNFKKEIKALVLTCCQSAPLESEHPLSTVHTVEVSKGSLRSGRSNPI 375
Db 314 VNPFIYGLNKNFORDLQFFNFCDFRSRDDDYETIAMSTMHTDVSKTSLK---QASPV 369

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RESULT 15

US-08-415-818-6
 Sequence 6, Application US/08415818
 Patent No. 5621079
 GENERAL INFORMATION:
 APPLICANT: Cascieri, Margaret A.
 APPLICANT: Linemeyer, David L.
 APPLICANT: MacNeil, Douglas J.
 APPLICANT: Shiao, Lin-Lin
 APPLICANT: Strader, Catherine D.
 APPLICANT: Tan, Carina P.
 APPLICANT: Weinberg, David H.

Search completed: May 11, 2004, 12:58:03
Job time : 24 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2004, 12:55:33 ; Search time 48 Seconds
(without alignments)
2168.490 Million cell updates/sec

Title: US-09-430-775-2

Perfect score: 1965
Sequence: 1 MNTSHLLALLPKSPQGENR.....TVHTEVSKGSLRSLGRSNPI 375

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1140673 seqs, 277566755 residues

Total number of hits satisfying chosen parameters: 1140673

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1965	100.0	375	9	US-09-962-646-17
2	1965	100.0	375	12	Sequence 17, Appl
3	1965	100.0	375	14	Sequence 12, Appl
4	1519	77.3	375	14	US-10-225-567A-203
5	1494	76.0	375	12	Sequence 203, App
6	960	48.9	375	12	Sequence 47, Appl
7	922	46.9	374	12	Sequence 48, Appl
8	869	44.2	382	9	Sequence 51, Appl
9	867.5	44.1	383	12	Sequence 359, App
10	863	43.9	371	15	Sequence 3, Appl
11	860.5	43.8	384	9	Sequence 50, Appl
12	856.5	43.6	384	9	US-10-081-810-50
13	856.5	43.6	384	9	US-10-328-916-9
14	856.5	43.6	384	10	Sequence 15, Appl
15	856.5	43.6	384	12	Sequence 2, Appl
					Sequence 23, Appl
					Sequence 4, Appl
					Sequence 4, Appl
					Sequence 4, Appl

16	856.5	43.6	384	14	US-10-176-847-26	Sequence 26, Appl
17	856.5	43.6	384	14	US-10-225-567A-378	Sequence 378, App
18	856.5	43.6	384	14	US-10-309-815-10	Sequence 10, Appl
19	856.5	43.6	384	14	US-10-177-293-330	Sequence 330, App
20	856.5	43.6	384	14	US-10-060-369-10	Sequence 10, Appl
21	856.5	43.6	384	14	US-10-291-990-31	Sequence 31, Appl
22	856.5	43.6	384	14	US-10-126-764-10	Sequence 10, Appl
23	856.5	43.6	384	15	US-10-295-027-640	Sequence 640, App
24	856.5	43.6	384	15	US-10-295-027-746	Sequence 746, App
25	847	43.1	371	12	US-10-081-810-49	Sequence 49, Appl
26	846.5	43.1	389	12	US-10-181-906-6	Sequence 6, Appl
27	842.5	42.9	384	14	US-10-274-851-4	Sequence 4, Appl
28	603	30.7	227	13	US-10-044-592-69	Sequence 69, Appl
29	573	29.2	290	12	US-10-181-906-16	Sequence 16, Appl
30	573	29.2	290	14	US-10-225-567A-376	Sequence 376, App
31	561.5	28.6	383	9	US-09-771-956-27	Sequence 27, Appl
32	560.5	28.5	383	9	US-09-771-956-21	Sequence 25, Appl
33	557	28.3	395	9	US-09-771-956-25	Sequence 10, Appl
34	556.5	28.3	394	9	US-09-771-956-10	Sequence 17, Appl
35	556.5	28.3	394	12	US-10-410-648-17	Sequence 17, Appl
36	556.5	28.3	394	14	US-10-013-846-17	Sequence 17, Appl
37	538.5	27.4	394	14	US-10-274-851-17	Sequence 23, Appl
38	529	26.9	352	9	US-09-771-956-23	Sequence 26, Appl
39	522	26.6	341	9	US-09-771-956-26	Sequence 20, Appl
40	518	26.4	341	9	US-09-771-956-20	Sequence 22, Appl
41	517	26.3	508	9	US-09-771-956-22	Sequence 6, Appl
42	515	26.2	350	9	US-09-771-956-6	Sequence 9, Appl
43	506	25.8	499	9	US-09-771-956-9	Sequence 24, Appl
44	498	25.3	499	9	US-09-771-956-24	Sequence 12, Appl
45	485.5	24.7	370	13	US-10-044-592-12	

ALIGNMENTS

RESULT 1
US-09-962-646-17
; Sequence 17, Application US/09962646
; Patent No. US20020103123A1
; GENERAL INFORMATION: CHRISTOPHE P.G.
; APPLICANT: WEINSHANK, RICHARD L
; APPLICANT: WALKER, MARY W
; APPLICANT: BRANCHEK, THERESA
; TITLE OF INVENTION: MODIFYING FEEDING BEHAVIOR, COMPOUNDS USEFUL IN SUCH METHODS, AND
; TITLE OF INVENTION: ENCODING A HYPOTHALAMIC ATYPICAL NEUROPEPTIDE Y/PEPTIDE YY RECEPTOR
; FILE REFERENCE: 1795/46166BZA
; CURRENT APPLICATION NUMBER: US/09/962,646
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/200,673
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 08/566,096
; PRIOR FILING DATE: 1995-12-01
; PRIOR APPLICATION NUMBER: 08/349,025
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-962-646-17

Query Match	100.0%	Score 1965;	DB 9;	Length 375;
Best Local Similarity	100.0%;	Pred. No. 5.8e-170;		
Matches 375;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MNTSHLLALLPKSPQGENSKPLGTPYNSHQCDSVDYVWVFTVTSYLETVVGLNGL	60	
DB	1	MNTSHLLALLPKSPQGENSKPLGTPYNSHQCDSVDYVWVFTVTSYLETVVGLNGL	60	
QY	61	CLMCTVROKQEKANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGFTLCKMSAPI	120	

Db 61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYIMDYWIFGETLCKMSAFI 120
Qy 121 QCMSTVTSILSLVALERHQLINPTGKPSISQAYLGIVLIWVIAVLSLPLFANSIL 180
Db 121 QCMSTVTSILSLVALERHQLINPTGKPSISQAYLGIVLIWVIAVLSLPLFANSIL 180
Qy 181 ENVFHKNHSALEFLADKVVCTESWPLAHRTIYITFTLLFOYCLPLGFIIVCYARIYR 240
Db 181 ENVFHKNHSALEFLADKVVCTESWPLAHRTIYITFTLLFOYCLPLGFIIVCYARIYR 240
Qy 241 LQRCGRVFHKGTYSLRAGHKQNVNVLVVMVAVAVLWPLPHVFNLSLEDMHHEAIPICHG 300
Db 241 LQRCGRVFHKGTYSLRAGHKQNVNVLVVMVAVAVLWPLPHVFNLSLEDMHHEAIPICHG 300
Qy 301 NLIFLVCHLLAMASTCNPFIYGFINTNFKEIKALVLTCCQSAPLESEHPLSTVHTE 360
Db 301 NLIFLVCHLLAMASTCNPFIYGFINTNFKEIKALVLTCCQSAPLESEHPLSTVHTE 360
Qy 361 VSKGSLRLSGRSNPI 375
Db 361 VSKGSLRLSGRSNPI 375

RESULT 2

US-10-181-906-12
; Sequence 12, Application US/10181906
; Publication No. US20040053864A1
; GENERAL INFORMATION:
; APPLICANT: Karsenty, Gerard
; APPLICANT: Amling, Michael
; APPLICANT: Dacy, Patricia
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROL OF BONE FORMATION VIA
; TITLE OF INVENTION: MODULATION OF NEUROPEPTIDE Y ACTIVITY
; FILE REFERENCE: 9142-020-999
; CURRENT APPLICATION NUMBER: US/10/181,906
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: PCT/US01/02040
; PRIOR FILING DATE: 2001-01-22
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-181-906-12

Query Match 100.0%; Score 1965; DB 12; Length 375;
Best Local Similarity 100.0%; Pred. No. 5.8e-170;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNTSHLLALLPKSPQGENRSKPLGTPYNFSEHCQSDVDVMVFIVTSYIETVVGVLGNL 60
Db 1 MNTSHLLALLPKSPQGENRSKPLGTPYNFSEHCQSDVDVMVFIVTSYIETVVGVLGNL 60
Qy 61 CLMCVTVRQKEKANVTNLLIANLAFSDFLMCLLCQPLTAVYIMDYWIFGETLCKMSAFI 120
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Db 241 LQRCGRVFHKGTYSLRAGHKQNVNVLVVMVAVAVLWPLPHVFNLSLEDMHHEAIPICHG 300
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Db 301 NLIFLVCHLLAMASTCNPFIYGFINTNFKEIKALVLTCCQSAPLESEHPLSTVHTE 360

Qy 361 VSKGSLRLSGRSNPI 375
Db 361 VSKGSLRLSGRSNPI 375
RESULT 3
US-10-225-567A-203
; Sequence 203, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burkner, Glenn A.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 203
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-203

Query Match 100.0%; Score 1965; DB 14; Length 375;
Best Local Similarity 100.0%; Pred. No. 5.8e-170;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 241 LQRCGRVFHKGTYSLRAGHKQNVNVLVVMVAVAVLWPLPHVFNLSLEDMHHEAIPICHG 300
Qy 301 NLIFLVCHLLAMASTCNPFIYGFINTNFKEIKALVLTCCQSAPLESEHPLSTVHTE 360
Db 301 NLIFLVCHLLAMASTCNPFIYGFINTNFKEIKALVLTCCQSAPLESEHPLSTVHTE 360
Qy 361 VSKGSLRLSGRSNPI 375
Db 361 VSKGSLRLSGRSNPI 375

RESULT 4

US-10-081-810-47
; Sequence 47, Application US/10081810
; Publication No. US20030064438A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR NUCLEIC ACIDS, POLYPEPTIDES, ANTIBODIES
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: D0132 NP
; CURRENT APPLICATION NUMBER: US/10/081,810
; CURRENT FILING DATE: 2002-02-22

105 OCMSVTS:FSMWLIALERHOLIHTPTGKVPVRHSYLAVAVIWIACFISLPISFNIL 164

QY 181 ENVFHKNHSALEFLADKVVCTESWPLAHRHTYTTTLLFOYCLPLGLVLCYARIVER 240
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; ORGANISM: Gadus morhua
US-10-072-012-359
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; TYPE: PRT
; ORGANISM: Gadus morhua
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; ORGANISM: Gadus morhua
US-10-072-012-359
Db 225 LSRKQWVERARGORQKAKGSKRVNAMLASIVAAFALOWPLNVFNTIFDWNHEAIPVC 284
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Gadus morhua
US-10-072-012-359
QY 299 HGNLIFLVCHLLAMASCNVPFIYGPLNTNFKKEIKALVLTCCOSAPLESSEHPLSTVH 358
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Gadus morhua
US-10-072-012-359
Db 285 OHDAIFSACHTTAVASTCVNPNVYGFPLNNFQKELSLSRRCRCWGPASSYSFPLSTVS 344
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Gadus morhua
US-10-072-012-359
QY 359 TEVSKGSLRLSGRSN 373
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Gadus morhua
US-10-072-012-359
Db 345 TGITKGSILNGSGS 359
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Gadus morhua
US-10-072-012-359

RESULT 7

US-10-072-012-359
; Sequence 359, Application US/10072012
; Publication No. US2004003493A1
; GENERAL INFORMATION:
; APPLICANT: Tcheinev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zernhusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Baba
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 359

QY 32 EHCQSDVDVWVFIYVTSIETVGVGLNCLMCTVTVQKSKANVTNLLIANLAFSDFLMC 91
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Gadus morhua
US-10-072-012-359
Db 28 BECPSSKSGTFLILVYSTMTIANGVIGNSCLFVFIARQKEMHNTNFIANLSCDILMC 87
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Gadus morhua
US-10-072-012-359
QY 92 LLCPLTAVYTIMDYWIFGETLCKMSAFICQMSVTVSILSLVALRHHOIIINPTGKWP 151
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Gadus morhua
US-10-072-012-359
Db 88 IFCLPVTIIVTMDRNLGEALCKLTFVQCISVTVSIFSLVJAMERYQIIIHPTGKWP 147
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Gadus morhua
US-10-072-012-359
QY 152 SISQAYGIVLIWVIACVLSLPLANSILENVFHHNSKALEFLA--DKVCTESWPLAHH 210
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Gadus morhua
US-10-072-012-359
Db 148 MVGOSYMAVGIIWVAVCLISVFLSFTVLDNLPLQNL--LPFFQDHWLCTESWPTNSN 205
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Gadus morhua
US-10-072-012-359
QY 211 RTIYTTLLFOYCLPLGLVLCYARIVRRLORGRVFKGTYSIRAGHMK--QVNVVL 267
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Gadus morhua
US-10-072-012-359
Db 206 RLAVTTSLLVFOYFELPLGLIAACVLSIFLRLRRKDWVERADSSRDNRKSGRRINVL 265
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Gadus morhua
US-10-072-012-359
QY 268 VMVAVFAVLWLPJHVFNSLEDHHEAIPICHGNLIFLVCHLLAMASTCVNPFYIGFLT 327
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Gadus morhua
US-10-072-012-359
Db 266 GSIVAFVAVCWPLNINFTVDFMHHLMVSCQNLIFSVCHLVANASTCVNPFVYVGLNS 325
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Gadus morhua
US-10-072-012-359
QY 328 NFKKEIKALVLTCCOSAPLESSEHPLSTVHTEV-----SKGSLRL 368
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Gadus morhua
US-10-072-012-359
Db 326 NFKQKATLSHCRWCWGAARYENLPLSAVSTEVTKESHMSKGSISI 372
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Gadus morhua
US-10-072-012-359

RESULT 8

US-09-771-956-3
; Sequence 3, Application US/09771956
; Patent No. US20010031474A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Michele
; APPLICANT: Brodbeck, Robbin
; APPLICANT: Krause, James
; TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors
; FILE REFERENCE: N2000, 001
; CURRENT APPLICATION NUMBER: US/09/771,956
; CURRENT FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-771-956-3
Query Match 44.2%; Score 869; DB 9; Length 382;
Best Local Similarity 46.8%; Pred. No. 1.9e-70;
Matches 168; Conservative 74; Mismatches 101; Indels 16; Gaps 4;
QY 28 YNFSEH-----CODSDVDMVFIYVTSIETVGVGLNCLMCTVTVQKSKANVTN 77
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-771-956-3
Db 16 YNVSENSPLAFENDDDCHLPLAVITLALAYGAVIILGVSGLNLAIIILKQKEMRNVTN 75
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-771-956-3
QY 78 LLIANLAFSDFLMCLLCOPLTAVYTIMDYWIFGETLCKMSAFICQMSVTVSILSLVAL 137
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-771-956-3
Db 76 ILIVNLSFSDLLVAVMCLPFFVTVTMDHWVFGTMCKLNPFCVSTVTSIFSLVLIIV 135
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-771-956-3
QY 138 ERHOLIINPTGKWSISQAYIGIVLIWVIACVLSLPLANSILENVFHHNSKALEFLAD 197
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-771-956-3
Db 136 ERHOLIINPTGKWSISQAYIGIVLIWVIACVLSLPLANSILENVFHHNSKALEFLAD 193
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-771-956-3
QY 198 KVVCTESWPLAHRHTYTTTLLFOYCLPLGLVLCYARIVRRLORGRVFKGTYS--LAAPD 256
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-771-956-3
Db 194 KVVCFDKFSDSHRLSYTLLLVLYQFGLPLCFIYFKIVIRLKRNNMMDKIRDSKYR 253
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-771-956-3

;; PRIOR FILING DATE: 1994-12-01
;; NUMBER OF SEQ ID NOS: 17
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 15
;; LENGTH: 384
;; TYPE: PRT
;; ORGANISM: Homo Sapiens
US-09-962-646-15

Query Match 43.8%; Score 860.5; DB 9; Length 384;
Best Local Similarity 44.9%; Pred. No. 1.1e-69;
Matches 167; Conservative 77; Mismatches 107; Indels 21; Gaps 5;

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QY 16 QGENRSKPLGTPYNFSE-----HCQDSVDVMVFIVTSYSIETVVGVLGNLCLMC 64
DB 8 QVENHS-----VHSNFSEKNAQLAFENDDDCHLPLAMIFTLALAYGAVIILGVSGNALII 63

QY 65 VTVRQEKANVTNLLIANLAFSDFLMCLLCQPLTAVTYTMDYWIYFGETLCKMSAFIQMS 124
DB 64 IILKQEMRNVTNLLIVNLSFSDLLVAIMCLPFTFVTLMDHWVFGAMCKLPFPVQCVS 123

QY 125 VTVSILSLVALERHQLIINPTGKWPISQAYLGIWLVIAVLSLPLANSILENVF 184
DB 124 ITVSIFSLVLIIVERHQLIINPRGWRNRRHAYVGLAVIWLAVASSLPFLIYQWMTDEP 183

QY 185 HKHNSKALEFLADKVCWCTESWPLAHRHTIYTTFLLLFYQYCLPLGFLVCYARIYRLQK 244
DB 184 FQN--VTLDAYKDYKVCDFQPSDSHRLSYTTLLLVLYQYFGLPCFIFYFYKVIYRLKRR 241

QY 245 GRVPHK-GTYSLRAGHKQNVNVLVWVAFVAVLWPLPLHVFNSLEWDHHEAIPICHGNLI 303
DB 242 NMMDKMRDNKYSRSETKRINIMLLSIVVAFVAVCWMLPTITFNTVFDWNHQIATCNHLL 301

QY 304 FLVCHLLAMASTCNPPIYGFNLNFKKEIKALVLTCCQSAPLESEHPLSTVHTVEVSK 363
DB 302 FLCHLTAMISTCNPPIYGFNLNFKFORDLQFFNFCDFRSDDDYETIAMSTMHTDVS 361

QY 364 GSLRLSGRSNPI 375
DB 362 TSLK---QASEV 370
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RESULT 12
US-09-771-956-2

;; Sequence 2, Application US/09771956
;; Patent No. US20010031474A1
;; GENERAL INFORMATION:
;; APPLICANT: Bennett, Michele
;; APPLICANT: Brodbeck, Robbin
;; APPLICANT: Krause, James
;; TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors
;; FILE REFERENCE: N2000.001
;; CURRENT APPLICATION NUMBER: US/09/771.956
;; CURRENT FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 31
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 2
;; LENGTH: 384
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-771-956-2

Query Match 43.6%; Score 856.5; DB 9; Length 384;
Best Local Similarity 44.6%; Pred. No. 2.6e-69;
Matches 166; Conservative 77; Mismatches 108; Indels 21; Gaps 5;

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QY 16 QGENRSKPLGTPYNFSE-----HCQDSVDVMVFIVTSYSIETVVGVLGNLCLMC 64
DB 8 QVENHS-----VHSNFSEKNAQLAFENDDDCHLPLAMIFTLALAYGAVIILGVSGNALII 63

QY 65 VTVRQEKANVTNLLIANLAFSDFLMCLLCQPLTAVTYTMDYWIYFGETLCKMSAFIQMS 124
DB 64 IILKQEMRNVTNLLIVNLSFSDLLVAIMCLPFTFVTLMDHWVFGAMCKLPFPVQCVS 123
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QY 125 VTVSILSLVALERHQLIINPTGKWPISQAYLGIWLVIAVLSLPLANSILENVF 184
DB 124 ITVSIFSLVLIIVERHQLIINPRGWRNRRHAYVGLAVIWLAVASSLPFLIYQWMTDEP 183

QY 185 HKHNSKALEFLADKVCWCTESWPLAHRHTIYTTFLLLFYQYCLPLGFLVCYARIYRLQK 244
DB 184 FQN--VTLDAYKDYKVCDFQPSDSHRLSYTTLLLVLYQYFGLPCFIFYFYKVIYRLKRR 241

QY 245 GRVPHK-GTYSLRAGHKQNVNVLVWVAFVAVLWPLPLHVFNSLEWDHHEAIPICHGNLI 303
DB 242 NMMDKMRDNKYSRSETKRINIMLLSIVVAFVAVCWMLPTITFNTVFDWNHQIATCNHLL 301

QY 304 FLVCHLLAMASTCNPPIYGFNLNFKKEIKALVLTCCQSAPLESEHPLSTVHTVEVSK 363
DB 302 FLCHLTAMISTCNPPIYGFNLNFKFORDLQFFNFCDFRSDDDYETIAMSTMHTDVS 361

QY 364 GSLRLSGRSNPI 375
DB 362 TSLK---QASEV 370
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RESULT 13
US-09-393-696-23
;; Sequence 23, Application US/09393696
;; Publication No. US20030022277A1
;; GENERAL INFORMATION:
;; APPLICANT: Human Genome Sciences, Inc. et al.
;; TITLE OF INVENTION: Human Neuropeptide Receptor
;; FILE REFERENCE: PFI68P2
;; CURRENT APPLICATION NUMBER: US/09/393.696
;; CURRENT FILING DATE: 1999-09-10
;; EARLIER APPLICATION NUMBER: PCT/US95/05616
;; EARLIER FILING DATE: 1995-05-05
;; EARLIER APPLICATION NUMBER: US08/462,509
;; EARLIER FILING DATE: 1995-06-05
;; NUMBER OF SEQ ID NOS: 23
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 23
;; LENGTH: 384
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-393-696-23

Query Match 43.6%; Score 856.5; DB 10; Length 384;
Best Local Similarity 44.6%; Pred. No. 2.6e-69;
Matches 166; Conservative 77; Mismatches 108; Indels 21; Gaps 5;

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QY 16 QGENRSKPLGTPYNFSE-----HCQDSVDVMVFIVTSYSIETVVGVLGNLCLMC 64
DB 8 QVENHS-----VHSNFSEKNAQLAFENDDDCHLPLAMIFTLALAYGAVIILGVSGNALII 63

QY 65 VTVRQEKANVTNLLIANLAFSDFLMCLLCQPLTAVTYTMDYWIYFGETLCKMSAFIQMS 124
DB 64 IILKQEMRNVTNLLIVNLSFSDLLVAIMCLPFTFVTLMDHWVFGAMCKLPFPVQCVS 123

QY 125 VTVSILSLVALERHQLIINPTGKWPISQAYLGIWLVIAVLSLPLANSILENVF 184
DB 124 ITVSIFSLVLIIVERHQLIINPRGWRNRRHAYVGLAVIWLAVASSLPFLIYQWMTDEP 183

QY 185 HKHNSKALEFLADKVCWCTESWPLAHRHTIYTTFLLLFYQYCLPLGFLVCYARIYRLQK 244
DB 184 FQN--VTLDAYKDYKVCDFQPSDSHRLSYTTLLLVLYQYFGLPCFIFYFYKVIYRLKRR 241

QY 245 GRVPHK-GTYSLRAGHKQNVNVLVWVAFVAVLWPLPLHVFNSLEWDHHEAIPICHGNLI 303
DB 242 NMMDKMRDNKYSRSETKRINIMLLSIVVAFVAVCWMLPTITFNTVFDWNHQIATCNHLL 301

QY 304 FLVCHLLAMASTCNPPIYGFNLNFKKEIKALVLTCCQSAPLESEHPLSTVHTVEVSK 363
DB 302 FLCHLTAMISTCNPPIYGFNLNFKFORDLQFFNFCDFRSDDDYETIAMSTMHTDVS 361

QY 364 GSLRLSGRSNPI 375
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```

; GENERAL INFORMATION:
; APPLICANT: Bakthavatchalam, Rajagopal
; APPLICANT: Blum, Charles A
; APPLICANT: Brielmann, Harry L
; APPLICANT: Darrow, James W
; APPLICANT: De Lombaert, Stephane
; APPLICANT: Hutchison, Alan
; APPLICANT: Tran, Jennifer
; APPLICANT: Zheng, Xiaozhang
; APPLICANT: Elliott, Richard L
; APPLICANT: Hammond, Mariys
; TITLE OF INVENTION: Spiro(isobenzofuran-1,4'-piperidin)-3-ones and
; TITLE OF INVENTION: 3H-spiro(isobenzofuran-1,4'-piperidines
; FILE REFERENCE: N00.2001
; CURRENT APPLICATION NUMBER: US/10/013,846
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: US 60/254,990
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 384
; TYPE: PR1
; ORGANISM: homosapiens
US-10-013-846-4

Query Match 43.6%; Score 856.5; DB 14; Length 384;
Best Local Similarity 44.6%; Pzed. No. 2.6e-69;
Matches 166; Conservative 77; Mismatches 108; Indels 21; Gaps 5;

Qy 16 QGNNRKPGLTPNPNSE-----HCQSDVMQVFIVTSYSEIYVGVGLNCLMC 64
Db 8 QVENHS-----VHSNFSKQAQLAFENDPDCHLPLAMIFTLALAYGAVILGVSGNLAI 63

Qy 65 VTVROKEKANTNLLITANLAFSDFLMCLLCOPLTAVYITMDYIMFGETLCKMSAFIQMS 124
Db 64 IILQKEMRVNLLIVNFSFDLLVAIMCLPFTFYITLNDHWFGKAMKLNPFQCVS 123

Qy 125 VTVSILSLVALERHQLIINPTGWKXPSIQAYGLGVLIVTWIACVLSLPLANSILENVF 184
Db 124 ITVSIFSLVIAVERHQLIINPRGWRPNRHXVGIWVLAVASSLPFLIYQVMTDF 183

Qy 185 HKHNSKALEFLADKVVCTESWPLAHERHTYTTFTLLLFQYCLPGLFIVCYARIYRLOQ 244
Db 184 FQN--VTLDAYKQKVCYCFDQFSDSHRLSYTTLLLVLFQGLPCLFFICYFKIYRLKR 241

Qy 245 GRVPHK--GTYSLRAGHKQNVVLVVMVAVFLWPLHVFVNSLEDWHHEAIPICHGNI 303
Db 242 NNMMDKVRDNKYRSSETKRINIMLSIVVAFACVCLPLPTIENFVDWNHQLIATCNHLL 301

Qy 304 FLVCHLLAMASTCVNPIFYGLNTNPKKELKALVLTQCSAPLESEHPLPLSTVHTEVSK 363
Db 302 PLLCHLTAMISTCVNPIFYGLNKFNFQDQLQFFNFCDFSRDDDDYETIAMSTMHTDVK 361

Qy 364 GSLRLSGRSNPI 375
Db 362 TSLK---QASPV 370

Search completed: May 11, 2004, 13:05:05
Job time : 49 secs

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Search completed: May 11, 2004, 13:05:05
Job time : 49 secs

RESULT 15
US-10-013-846-4
; Sequence 4, Application US/10013846
; Publication No. US20030036652A1

RESULT 15
US-10-013-846-4
; Sequence 4, Application US/10013846
; Publication No. US20030036652A1